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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 23433 Seconds
(without alignments)
17657.111 Million cell updates/sec

Title: US-09-275-883-1_COPY_1_8539

Perfect score: 8539
Sequence: 1 ctgacgcgcctgttagcgcc.....atactaacaccaccacct 8539

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_hhg:*
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6: gb_pac:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8539	100.0	11282	6 BD203630	BD203630 Inducible
2	8539	100.0	11282	6 CQ790428	CQ790428 Sequence
3	8539	100.0	11282	6 AR342585	AR342585 Sequence
4	8539	100.0	11282	6 AX128601	AX128601 Sequence
5	8539	100.0	11282	6 AX174827	AX174827 Sequence
6	7657.2	89.7	13068	6 CQ790429	CQ790429 Sequence
7	7657.2	89.7	15081	6 CQ790448	CQ790448 Sequence
8	7657.2	89.7	17753	6 CQ790449	CQ790449 Sequence
9	7637.4	89.4	9951	6 AR282858	AR282858 Sequence
10	7637.4	89.4	9951	6 AX128602	AX128602 Sequence
11	7637.4	89.4	10524	6 AR282859	AR282859 Sequence
12	7637.4	89.4	11927	6 AR282860	AR282860 Sequence
13	7637.4	89.4	13905	6 AR137241	AR137241 Sequence
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16	7634.8	89.4	8000	6 AR230676	AR230676 Sequence
17	7634.8	89.4	8000	6 AR234150	AR234150 Sequence
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19	7634.8	89.4	8000	6 AR353270	AR353270 Sequence

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21	7634.8	89.4	8000	6 BD085671	BD085671 Recombina
22	7634.8	89.4	11703	14 SINGC	J02363 Sindbis vir
23	7634.8	89.4	11740	6 AR221250	AR221250 Sequence
24	7634.8	89.4	11740	6 AR230677	AR230677 Sequence
25	7634.8	89.4	11740	6 AR234151	AR234151 Sequence
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31	7620.4	89.2	11703	6 BD269911	BD269911 Compositi
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38	7617.2	89.2	8000	6 AR234149	AR234149 Sequence
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ALIGNMENTS

RESULT 1
BD203630 11282 bp DNA linear PAT 17-JUL-2003
LOCUS BD203630 Inducible alpha virus gene expression system.
DEFINITION BD203630
ACCESSION BD203630.1 GI:33013400
VERSION JP 2002509729-A/1.
KEYWORDS JP 2002509729-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 11282)
AUTHORS Renner,W.A., Nieba,L. and Boorsma,M.
TITLE Inducible alpha virus gene expression system
JOURNAL Patent: JP 2002509729-A 1 02-APR-2002;
CYTOS BIOTECHNOLOGY AG
COMMENT OS Artificial Sequence
PN JP 2002509729-A/1
PD 02-APR-2002
PF 25-MAR-1999 JP 2000541320
PR 27-MAR-1998 US 60/079562
PI WOLFGANG A RENNEN, LARS NIEBA, MARCO BOORSMA
PC C12N15/09,A01K67/027,A61K48/00,C07K14/18,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12N7/04,C12N9/12,C12N15/00,C12N5/00 CC Description
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location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	6961	TATCCGAAACCATTTGTACTTCCAGTAGCGTACCAGCGAACTACTCCGATCCACAGTTGCT	7020
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QY	7681	ATTCAACACGCTTTTGACATGTGCGCGGAGAGATTTTGATGCAATCATAGCAGAACACTTC	7740
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Db	7741	AAGCAAGCGCAACCCGGTACTGGAGACGGATATCGCATCTTCGACAAAAGCCAAAGACGAC	7800
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Db	7801	GCTATGCGCTTAAACCGGTCTGATCTTGGAGAGACCTGGGTGGATCAACCACTACTC	7860
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Db	7861	GACTTGATCGAGTGCGCCCTTGGAGAAATATCATCCACCCTACTACGGGTACTCGT	7920
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Qy	8221	GTGCGGATCCCTCGAAAAGGCTGTTAAGTTGGGTAAACCGCTCCAGCGCAGCAGAG	8280
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Qy	8281	CAAGACGAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGCGTGTGTTAGAGTAGGT	8340
Db	8281	CAAGACGAGACAGAAGACGCGCTCTGCTAGATGAAACAAAGCGTGTGTTAGAGTAGGT	8340
Qy	8341	ATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCCGTATGAGGTAGACAATATTACACT	8400
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Qy	8401	GTCCTACTGGCATTGAGAACTTTGCCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG	8460
Db	8401	GTCCTACTGGCATTGAGAACTTTGCCCCAGAGCAAAAGAGCATTCCAAGCCATCAGAGGG	8460
Qy	8461	GAAATAAAGCATCTCTACGGTGTCTTAATAGTACAGATAGTACATTTCACTGACTAA	8520
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RESULT 2				
CQ790428				
LOCUS	CQ790428	11282 bp	DNA	linear
DEFINITION	Sequence 1 from Patent WO2004018506.			PAT 29-MAR-2004
ACCESSION	CQ790428			
VERSION	CQ790428.1	GI:45823470		
KEYWORDS	synthetic construct			
SOURCE	synthetic construct			
ORGANISM	other sequences; artificial sequences.			
REFERENCE	1			
AUTHORS	Ivanova,L., Renner,W.A. and Saudan,P.			
TITLE	Inducible alpha1viral/orip based gene expression system			
JOURNAL	Patent: WO 2004018506-A 1 04-MAR-2004;			

Cytos Biotechnology AG (CH)
Location/Qualifiers
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/mol_type="unassigned DNA"
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/note="cDNA"

ORIGIN

Query Match 100.0%; Score 8539; DB 6; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGACGCGCCCTGTAGCGCGGCATTAAGCGCGGGGTGTGTGTGTACGCGCAGCGTGA 60
QY 61 CCGCTACACTTGGCAGCGCCCTAGCGCCCGCTTCTTCCGCTTCTTCTTCTTCG 120
DB 61 CCGCTACACTTGGCAGCGCCCTAGCGCCCGCTTCTTCCGCTTCTTCTTCTTCG 120
QY 121 CCACGTTCCCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTCCGAT 180
DB 121 CCACGTTCCCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTCCGAT 180
QY 181 TTAGTGTCTTACGCGACCTCGACCCCAAAAATTGATTAGGGTGTGATGTTACGTAAGT 240
DB 181 TTAGTGTCTTACGCGACCTCGACCCCAAAAATTGATTAGGGTGTGATGTTACGTAAGT 240
QY 241 GGCCATCGCCCTGTATAGACGGTTTTCGCGCTTGAAGTTGAGTCCAGCTTCTTAATA 300
DB 241 GGCCATCGCCCTGTATAGACGGTTTTCGCGCTTGAAGTTGAGTCCAGCTTCTTAATA 300
QY 301 GTGACTCTTGTTCCAAACCTGGAACAACATCAACCCCTATCTCGGTCTATTCTTTGATT 360
DB 301 GTGACTCTTGTTCCAAACCTGGAACAACATCAACCCCTATCTCGGTCTATTCTTTGATT 360
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QY      841 TTCCGCAATTGCAGAGATATGTATTAAAGTCCCTACCTCGATACCGTGCAGATTGACGG 900
DB      841 TTCCGCAATTGCAGAGATATGTATTAAAGTCCCTACCTCGATACCGTGCAGATTGACGG 900
QY      901 CGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCACTAACCATCACAATGAGAAG 960
DB      901 CGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCACTAACCATCACAATGAGAAG 960
QY      961 CCAGTAGTAAACGTAGACGTAGACCCCAAGATCCGTTGTGCTGCAACTGCAAAAAAGC 1020
DB      961 CCAGTAGTAAACGTAGACGTAGACCCCAAGATCCGTTGTGCTGCAACTGCAAAAAAGC 1020
QY      1021 TTCCGCAATTTGAGGTAGTAGACACAGCAGTCACTCCAATGACCATGTAAATGCCAGA 1080
DB      1021 TTCCGCAATTTGAGGTAGTAGACACAGCAGTCACTCCAATGACCATGTAAATGCCAGA 1080
QY      1081 GCATTTTCGATCTGGCCAGTAACTAATCGAGCTGAGGTTCTTACCACAGCGCAGATC 1140
DB      1081 GCATTTTCGATCTGGCCAGTAACTAATCGAGCTGAGGTTCTTACCACAGCGCAGATC 1140
QY      1141 TTGACATAGGACGCGCACCGGCTCGTAGAATGTTTCCGAGCACCAAGTATCATTTGTGC 1200
DB      1141 TTGACATAGGACGCGCACCGGCTCGTAGAATGTTTCCGAGCACCAAGTATCATTTGTGC 1200
QY      1201 TGCCCCATGCGTAGTCCAGAAAGACCCGACCGCATGTAATAACGACAGTAACTGGCG 1260
DB      1201 TGCCCCATGCGTAGTCCAGAAAGACCCGACCGCATGTAATAACGACAGTAACTGGCG 1260
QY      1261 GAAAAAGCGTGCAAGATTACAAAACAAGACTTGATGAGAAGATTAAAGATCTCCGACC 1320
DB      1261 GAAAAAGCGTGCAAGATTACAAAACAAGACTTGATGAGAAGATTAAAGATCTCCGACC 1320
QY      1321 GTACTTGATACGCGGATGCTGAAACACCATGCTCTGTTTCAACAAGATTAACCTGC 1380
DB      1321 GTACTTGATACGCGGATGCTGAAACACCATGCTCTGTTTCAACAAGATTAACCTGC 1380
QY      1381 AACATGCGTCCGAATATTCCTCATATGACAGACGTATATCAACGCTCCCGAACTATC 1440
DB      1381 AACATGCGTCCGAATATTCCTCATATGACAGACGTATATCAACGCTCCCGAACTATC 1440
QY      1441 TATCATCAGGCTATGAAGCGGCTGCGGACCCCTGTACTGATTGGCTTCGACACCAACCAG 1500
DB      1441 TATCATCAGGCTATGAAGCGGCTGCGGACCCCTGTACTGATTGGCTTCGACACCAACCAG 1500
QY      1501 TTCAATGTTCTCGGCTATGGCAGGTTGTAACCTGCGTACCAACAACCACTGGGCGACGAG 1560
DB      1501 TTCAATGTTCTCGGCTATGGCAGGTTGTAACCTGCGTACCAACAACCACTGGGCGACGAG 1560
QY      1561 AAAGTCTTGAAGCGGTAACATCGACTTTCAGACCAAAAGCTGAGTGAAGTAGACA 1620
DB      1561 AAAGTCTTGAAGCGGTAACATCGACTTTCAGACCAAAAGCTGAGTGAAGTAGACA 1620
QY      1621 GGAATAATGTGATATGAGGAAGAGAGTTGAAGCCCGGTCGGGTTTATTCTCC 1680
DB      1621 GGAATAATGTGATATGAGGAAGAGAGTTGAAGCCCGGTCGGGTTTATTCTCC 1680
QY      1681 GTAGATCGACACTTATCCAGAACACAGACCAAGCTTGACAGAGCTGGCATCTTCCATCG 1740
DB      1681 GTAGATCGACACTTATCCAGAACACAGACCAAGCTTGACAGAGCTGGCATCTTCCATCG 1740
QY      1741 GTGTTCCACTTGAATGGAAGCAAGTCTGACACTTGCCGCTGTGATACAGTGTGAGTTGC 1800
DB      1741 GTGTTCCACTTGAATGGAAGCAAGTCTGACACTTGCCGCTGTGATACAGTGTGAGTTGC 1800
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QY 1801 GAAGGTTACGTAGTGAAGAAATCACCATCAGTCCCGGGATCACGGGAGAGAAACCCTGGGA 1860
|||
Db 1801 GAAGGTTACGTAGTGAAGAAATCACCATCAGTCCCGGGATCACGGGAGAGAAACCCTGGGA 1860
QY 1861 TACGGGGTTACACACAATAGCGAGGGCTTTCTGTCTATGCAAAATTACTGACACAGTAAAA 1920
|||
Db 1861 TACGGGGTTACACACAATAGCGAGGGCTTTCTGTCTATGCAAAATTACTGACACAGTAAAA 1920
QY 1921 GGAGAACGGGTATCGTTCCTGTGTGACGTACATCCCGGCCACCATATGCGATCAGATG 1980
|||
Db 1921 GGAGAACGGGTATCGTTCCTGTGTGACGTACATCCCGGCCACCATATGCGATCAGATG 1980
QY 1981 ACTGGTATTAATGGCCACGGATATATCACTGACGATGCACAAAACTTCTGTGGGCTC 2040
|||
Db 1981 ACTGGTATTAATGGCCACGGATATATCACTGACGATGCACAAAACTTCTGTGGGCTC 2040
QY 2041 AACCAAGCAATTGTCATTACGGTAGACTAACAGGAACACCAACCATGCAAAATTAC 2100
|||
Db 2041 AACCAAGCAATTGTCATTACGGTAGACTAACAGGAACACCAACCATGCAAAATTAC 2100
QY 2101 CTTCTGCGGATCATAGCACAAAGGTTCAAGCAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
|||
Db 2101 CTTCTGCGGATCATAGCACAAAGGTTCAAGCAATGGGCTAAGGAGCGCAAGGATGATCTT 2160
QY 2161 GATTAACGAAAAATGCTGGGTACTAGAAACGCAAGCTTACGTATGGCTGTTGTGGCG 2220
|||
Db 2161 GATTAACGAAAAATGCTGGGTACTAGAAACGCAAGCTTACGTATGGCTGTTGTGGCG 2220
QY 2221 TTTCGACTAAGAAAGTACATTGTTTTATCGCCACCTGGAACGACGACCTGCGTAAAA 2280
|||
Db 2221 TTTCGACTAAGAAAGTACATTGTTTTATCGCCCACTGGAACGACGACCTGCGTAAAA 2280
QY 2281 GTCCCAAGCTTTTAAAGCGCTTTTCCCATGTGCTCCGTATGAGACGACCTTTGGCCCATG 2340
|||
Db 2281 GTCCCAAGCTTTTAAAGCGCTTTTCCCATGTGCTCCGTATGAGACGACCTTTGGCCCATG 2340
QY 2341 TCGCTGAGGCAAGAAATTGAAACTGGCAATTGCCAACAAAGAGAGAGAAAACTGCTGCAG 2400
|||
Db 2341 TCGCTGAGGCAAGAAATTGAAACTGGCAATTGCCAACAAAGAGAGAGAAAACTGCTGCAG 2400
QY 2401 GTCTCGAGGAATTAGTCATGAGGCCAAGGCTGCTTTGAGGATGCTCAGAGGAAGCC 2460
|||
Db 2401 GTCTCGAGGAATTAGTCATGAGGCCAAGGCTGCTTTGAGGATGCTCAGAGGAAGCC 2460
QY 2461 AGAGCGGAGAACTCCGAGAGACCTTCCACCATTAGTGACAGACAAAGCATCGAGCA 2520
|||
Db 2461 AGAGCGGAGAACTCCGAGAGACCTTCCACCATTAGTGACAGACAAAGCATCGAGCA 2520
QY 2521 GCCGCAAGATTGTCTGCGAAGTGAAGGGCTCCAGGCGGACATCGGACGACATTAGTT 2580
|||
Db 2521 GCCGCAAGATTGTCTGCGAAGTGAAGGGCTCCAGGCGGACATCGGACGACATTAGTT 2580
QY 2581 GAAACCCCCCGCGGTCAAGTAAGATTAATCTCAAGCAAAATGACCGTATGATCGGACAG 2640
|||
Db 2581 GAAACCCCCCGCGGTCAAGTAAGATTAATCTCAAGCAAAATGACCGTATGATCGGACAG 2640
QY 2641 TATATCGTTGTCTCGCCAAACTGTGTGTAAGAAATGCCAAACTCGCACACGCCGCCG 2700
|||
Db 2641 TATATCGTTGTCTCGCCAAACTGTGTGTAAGAAATGCCAAACTCGCACACGCCGCCG 2700
QY 2701 CTAGCAGATCAGGTTAAGATCATAAACACTCCGGAAGATCAGAAAGTACGCGGTGAA 2760
|||
Db 2701 CTAGCAGATCAGGTTAAGATCATAAACACTCCGGAAGATCAGAAAGTACGCGGTGAA 2760
QY 2761 CCATACGACGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAGAAATTCCTA 2820
|||
Db 2761 CCATACGACGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAGAAATTCCTA 2820
QY 2821 GCACTGAGTGAAGCGCCACGTTAGTGTACAAAGAAAGAGAGTTGTGAAACCGCAAACTA 2880
|||
Db 2821 GCACTGAGTGAAGCGCCACGTTAGTGTACAAAGAAAGAGAGTTGTGAAACCGCAAACTA 2880
QY 2881 TACCACATGCGCATGATGCGCCCGCCAAAGATTAAGAAAGAGAGCAGTACAAAGTTACA 2940
|||

Db 2881 TACCACATGCGCATGATGCGCCCGCCAAAGATTAAGAAAGAGAGCAGTACAAAGTTACA 2940
QY 2941 AAGCAGAGCTTGCAAAAACAGATAGCTGTTTGACGTGACAGAAAGCGTTGCGTTAAG 3000
|||
Db 2941 AAGCAGAGCTTGCAAAAACAGATAGCTGTTTGACGTGACAGAAAGCGTTGCGTTAAG 3000
QY 3001 AAGGAAGAGCCTCAGGTCGTGCTCTCGGAGAACTGACCAACCTCCCTATCATGAG 3060
|||
Db 3001 AAGGAAGAGCCTCAGGTCGTGCTCTCGGAGAACTGACCAACCTCCCTATCATGAG 3060
QY 3061 CTAGCTTGAGGGGACTGAAGACCCGACCTGCGGTCCCGTACAGGTGGAACAATAGGA 3120
|||
Db 3061 CTAGCTTGAGGGGACTGAAGACCCGACCTGCGGTCCCGTACAGGTGGAACAATAGGA 3120
QY 3121 GTGATAGGCAACCGGGGTGCGGCAAGTCACTATTATCAAGTCAACTGTCAAGGACGA 3180
|||
Db 3121 GTGATAGGCAACCGGGGTGCGGCAAGTCACTATTATCAAGTCAACTGTCAAGGACGA 3180
QY 3181 GATCTTGTTAACAGCGGAAAGAAAGAAATTTGTCGCAAAATTGAGCGCGACGCTAAGA 3240
|||
Db 3181 GATCTTGTTAACAGCGGAAAGAAAGAAATTTGTCGCAAAATTGAGCGCGACGCTAAGA 3240
QY 3241 CTGAGGGGTAATGCAAGATTACGTGAAAGCAGTAGATTGCTTATGCTCAACGGATGCCAC 3300
|||
Db 3241 CTGAGGGGTAATGCAAGATTACGTGAAAGCAGTAGATTGCTTATGCTCAACGGATGCCAC 3300
QY 3301 AAAAGCCGTAGAAAGTGCTGTACGTTGACGAAGCGTTGCGGTGCCACGACGACACTACTT 3360
|||
Db 3301 AAAAGCCGTAGAAAGTGCTGTACGTTGACGAAGCGTTGCGGTGCCACGACGACACTACTT 3360
QY 3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAGGTAGTACTATGCGGAGACCCCATGCAA 3420
|||
Db 3361 GCCTTGATTGCTATCGTCAGGCCCCGCAAGAGGTAGTACTATGCGGAGACCCCATGCAA 3420
QY 3421 TCGGATTTCTCAACATGATGCAACTAAAGTACATTTCATACCCCTGAAAAAGACATA 3480
|||
Db 3421 TCGGATTTCTCAACATGATGCAACTAAAGTACATTTCATACCCCTGAAAAAGACATA 3480
QY 3481 TGACCAAGACATTTCTACAAGTATATCTCCGGCTTGACACACAGCCGTTACAGCTATT 3540
|||
Db 3481 TGACCAAGACATTTCTACAAGTATATCTCCGGCTTGACACACAGCCGTTACAGCTATT 3540
QY 3541 GTATGCACTGCTATTACGATGGAAGATGAAAAACCAAGAACCCGTGCAAGAAACATT 3600
|||
Db 3541 GTATGCACTGCTATTACGATGGAAGATGAAAAACCAAGAACCCGTGCAAGAAACATT 3600
QY 3601 GAAATCGATATTTACAGGGGCCAACAGCCGAAGCCAGGGGATATCATCTGACATGTTTC 3660
|||
Db 3601 GAAATCGATATTTACAGGGGCCAACAGCCGAAGCCAGGGGATATCATCTGACATGTTTC 3660
QY 3661 CGCGGTGGTTAAGCAATTGCAAAATCGACTATCCCGGACATGAAGTATGACAGCCGCG 3720
|||
Db 3661 CGCGGTGGTTAAGCAATTGCAAAATCGACTATCCCGGACATGAAGTATGACAGCCGCG 3720
QY 3721 GCCTCACAAGGCTAACCAAGAAAGAGTGTATGCCCTCCGCAAAAAGTCAATGAAAAAC 3780
|||
Db 3721 GCCTCACAAGGCTAACCAAGAAAGAGTGTATGCCCTCCGCAAAAAGTCAATGAAAAAC 3780
QY 3781 CCACTGTACGCGATCAATCAGAGCATGTGAACGTGTGCTCACCCGCACTGAGGACAGG 3840
|||
Db 3781 CCACTGTACGCGATCAATCAGAGCATGTGAACGTGTGCTCACCCGCACTGAGGACAGG 3840
QY 3841 CTAGTGTGAAAACTTGACGGGCGACCATGGAATTAAAGCAGCCCACTAACTAACCTAAA 3900
|||
Db 3841 CTAGTGTGAAAACTTGACGGGCGACCATGGAATTAAAGCAGCCCACTAACTAACCTAAA 3900
QY 3901 GAAACTTTACAGGCTACTATAGAGAGCTGGAAGCTGAACACAAAGGATTAATTGCTGCA 3960
|||
Db 3901 GAAACTTTACAGGCTACTATAGAGAGCTGGAAGCTGAACACAAAGGATTAATTGCTGCA 3960
QY 3961 ATAAACAGCCCACTCCCGGTGCCAATCCGTTCAAGCTGCAAGACCAAGCTTGTGGGCG 4020
|||

Db	3961	ATTAACAGCCCCACTCCCCCGTGCCAATCCGGTTCAGCTGCAAGACCAACGTTTGCTGGCG	4020
QY	4021	AAAGCATTTGGAAACCGATACTAGCCACGGCCGGTATCGTATTAACCGGTTGCCAGTGGAC	4080
Db	4021	AAAGCATTTGGAAACCGATACTAGCCACGGCCGGTATCGTATTAACCGGTTGCCAGTGGAC	4080
QY	4081	GAACTGTTCCCAACAGTTTGCGGATGACAAACCAACATTCGGCCATTTACGCCTTAGACGTA	4140
Db	4081	GAACTGTTCCCAACAGTTTGCGGATGACAAACCAACATTCGGCCATTTACGCCTTAGACGTA	4140
QY	4141	ATTTCATTAAAGTTTTTTCGGCATGGACTTGACAAAGCGGACTGTTTTCTAAACAGACATC	4200
Db	4141	ATTTCATTAAAGTTTTTTCGGCATGGACTTGACAAAGCGGACTGTTTTCTAAACAGACATC	4200
QY	4201	CCAATAACGTACCATCCCCGCCGATTCAGCCGAGGCCGGTAGCTCATTTGGACAACAGCCCA	4260
Db	4201	CCAATAACGTACCATCCCCGCCGATTCAGCCGAGGCCGGTAGCTCATTTGGACAACAGCCCA	4260
QY	4261	GGAACCCCGCAAGTATGGGTACGATCAAGCCATTGCGCGGAACTCTCCGTAGATTTCCG	4320
Db	4261	GGAACCCCGCAAGTATGGGTACGATCAAGCCATTGCGCGGAACTCTCCGTAGATTTCCG	4320
QY	4321	GTCGTTCCAGCTAGCTGGGAAGGGCACACAACCTGATTTGACAGCGGAGAACAGAGTT	4380
Db	4321	GTCGTTCCAGCTAGCTGGGAAGGGCACACAACCTGATTTGACAGCGGAGAACAGAGTT	4380
QY	4381	ATCTCTGCACAGCATAACTGGTCCCGGTGAACCGCAATCTTCCTCACGCCCTTAGTCCCC	4440
Db	4381	ATCTCTGCACAGCATAACTGGTCCCGGTGAACCGCAATCTTCCTCACGCCCTTAGTCCCC	4440
QY	4441	GAGTACAAGAGAGAACCAACCCGCCCGGTCABAAAAATTCTTGAAACCAAGTTCAACACCAC	4500
Db	4441	GAGTACAAGAGAGAACCAACCCGCCCGGTCABAAAAATTCTTGAAACCAAGTTCAACACCAC	4500
QY	4501	TCAGTACTTGTGATTCAGAGGAAAAAATTGAAAGTCCCCGTAAAGAAATCGAATGGATC	4560
Db	4501	TCAGTACTTGTGATTCAGAGGAAAAAATTGAAAGTCCCCGTAAAGAAATCGAATGGATC	4560
QY	4561	GCCCCGATTGGCATAGCCGGGTGCAATAGAAGTACAACCTGGCTTCCGGTTCCGCCG	4620
Db	4561	GCCCCGATTGGCATAGCCGGGTGCAATAGAAGTACAACCTGGCTTCCGGTTCCGCCG	4620
QY	4621	CAGGCACGGTACGACCTGGTGTTCATCAACATTTGGAATAAATACAGAAAACCAACTTT	4680
Db	4621	CAGGCACGGTACGACCTGGTGTTCATCAACATTTGGAATAAATACAGAAAACCAACTTT	4680
QY	4681	CAGCAGTGCGAAGACCAATGGCGGCACTTAATAAACCTTTCGCCGTTCCGCCCTGAATTGT	4740
Db	4681	CAGCAGTGCGAAGACCAATGGCGGCACTTAATAAACCTTTCGCCGTTCCGCCCTGAATTGT	4740
QY	4741	TTAAACTCAGAGGCAACCTCGTGTGTGAAGTCTTAATGCTACGCCGACCCGCAACAGTGAG	4800
Db	4741	TTAAACTCAGAGGCAACCTCGTGTGTGAAGTCTTAATGCTACGCCGACCCGCAACAGTGAG	4800
QY	4801	GACGTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAAGTTGT	4860
Db	4801	GACGTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAGGGTGTCTGCAGCGAGACCAAGTTGT	4860
QY	4861	GTCCTCAAGCAATACAGAAATGTACTCTGATTTTCCGACAACCTAGACAACAGCCGTACACGG	4920
Db	4861	GTCCTCAAGCAATACAGAAATGTACTCTGATTTTCCGACAACCTAGACAACAGCCGTACACGG	4920
QY	4921	CAATTCAACCCCGCACCACTCTGAATTGCGTGAATTCGTCGCTGATGAGGGTACAAGAGAT	4980
Db	4921	CAATTCAACCCCGCACCACTCTGAATTGCGTGAATTCGTCGCTGATGAGGGTACAAGAGAT	4980
QY	4981	GGAGTTGAGCCGCGCGCTCATACCGCACCAAAAGGAGAAATATTGCTGACTGTCAAGAG	5040
Db	4981	GGAGTTGAGCCGCGCGCTCATACCGCACCAAAAGGAGAAATATTGCTGACTGTCAAGAG	5040
QY	5041	GAAAGCATTTGTCAACGCAACCAATCCGCTGGGTAGACCAAGCGAAGAGTCTGCCGTGCC	5100
Db	5041	GAAAGCATTTGTCAACGCAACCAATCCGCTGGGTAGACCAAGCGAAGAGTCTGCCGTGCC	5100

QY	5101	ATCTATAAACGTTGGCCCGACCAGTTTACCATTACGCCACGGAGACAGGCACCGCAGA	5160
Db	5101	ATCTATAAACGTTGGCCCGACCAGTTTACCATTACGCCACGGAGACAGGCACCGCAGA	5160
QY	5161	ATGACTGTGTGCTTAGGAAAGAAAGTATCCACGCGGTGCGCCCTGATTTCCGGAAGCAC	5220
Db	5161	ATGACTGTGTGCTTAGGAAAGAAAGTATCCACGCGGTGCGCCCTGATTTCCGGAAGCAC	5220
QY	5221	CCAGAAGCAGAAAGCCTTGAAATTTGTCACAAAACGCTACCATGACAGTGCGACACTTAGTA	5280
Db	5221	CCAGAAGCAGAAAGCCTTGAAATTTGTCACAAAACGCTACCATGACAGTGCGACACTTAGTA	5280
QY	5281	AATGAACATAACATCAAGTCTGTGCGCATTTCCACTGCTATCTACAGGCATTTACGACGCC	5340
Db	5281	AATGAACATAACATCAAGTCTGTGCGCATTTCCACTGCTATCTACAGGCATTTACGACGCC	5340
QY	5341	GGAAGAAGACCGCCTTGAAGTATCACTTAACCTGCTTGACAAACCGCCTAGACAGAACTGAC	5400
Db	5341	GGAAGAAGACCGCCTTGAAGTATCACTTAACCTGCTTGACAAACCGCCTAGACAGAACTGAC	5400
QY	5401	GCGGACGTAAACCATCTATTGCTGCTGATTAAGAAGTGAAGGAAGAATCGACGCGGCACTC	5460
Db	5401	GCGGACGTAAACCATCTATTGCTGCTGATTAAGAAGTGAAGGAAGAATCGACGCGGCACTC	5460
QY	5461	CAACTTAAGAGTCTGTAAACAGAGCTGAAGGATGAAGATATGAGATCGACGATGAGTTA	5520
Db	5461	CAACTTAAGAGTCTGTAAACAGAGCTGAAGGATGAAGATATGAGATCGACGATGAGTTA	5520
QY	5521	GATGATTCATCCAGACAGTTGCTGAAGGGAAGAAAGGATTCACTACATAAAAGGA	5580
Db	5521	GATGATTCATCCAGACAGTTGCTGAAGGGAAGAAAGGATTCACTACATAAAAGGA	5580
QY	5581	AAATTGATTCGTACTTCGAAGGCAACAAATTCATCAAGCAGCAAAAGACATGGCGGAG	5640
Db	5581	AAATTGATTCGTACTTCGAAGGCAACAAATTCATCAAGCAGCAAAAGACATGGCGGAG	5640
QY	5641	ATTAAGGTCTGTTCCCTAATGACCAAGAAAGTAATGAACAATGTGTGCTACATATTG	5700
Db	5641	ATTAAGGTCTGTTCCCTAATGACCAAGAAAGTAATGAACAATGTGTGCTACATATTG	5700
QY	5701	GGTGAGACCATGGAAGCAATCCGCGAATAAGTGCCCGGTCCAGCCATTAACCCGTCCTAGC	5760
Db	5701	GGTGAGACCATGGAAGCAATCCGCGAATAAGTGCCCGGTCCAGCCATTAACCCGTCCTAGC	5760
QY	5761	CCGCCCAAAACGTTGCCGTGCTTTGCAATGATGCCATGAACGCCAGAAAGGTCACACAGA	5820
Db	5761	CCGCCCAAAACGTTGCCGTGCTTTGCAATGATGCCATGAACGCCAGAAAGGTCACACAGA	5820
QY	5821	CTTAGAAGCAATTAACGTCAAAAGATTACAGTATGCTCTCCACCCCTTCCTTAAGCAC	5880
Db	5821	CTTAGAAGCAATTAACGTCAAAAGATTACAGTATGCTCTCCACCCCTTCCTTAAGCAC	5880
QY	5881	AAAAATTAAAGATGTTCAAGAGTTCACTGACAGAAAGTAGTCTGTTTAAATCCGCACACT	5940
Db	5881	AAAAATTAAAGATGTTCAAGAGTTCACTGACAGAAAGTAGTCTGTTTAAATCCGCACACT	5940
QY	5941	CCCGCATTCGTTCCCGCCCGCTAAGTACATAGAAGTCCAGAACAGCCTACCGCTCCTCCT	6000
Db	5941	CCCGCATTCGTTCCCGCCCGCTAAGTACATAGAAGTCCAGAACAGCCTACCGCTCCTCCT	6000
QY	6001	GCACAGGCGGAGAGGCCCGGAAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC	6060
Db	6001	GCACAGGCGGAGAGGCCCGGAAAGTTGTAGCGACACCGTCACCATCTACAGCTGATAAC	6060
QY	6061	ACCTCGTTGATGTCAACAGATCTCACTGATATGGAATGACAGTAGCGAAGGCTCACTT	6120
Db	6061	ACCTCGTTGATGTCAACAGATCTCACTGATATGGAATGACAGTAGCGAAGGCTCACTT	6120
QY	6121	TTTTTCGAGCTTTAGCGGATCGGACAACTCTATTAAGTATGACAGATTGCTGTCAAGGA	6180
Db	6121	TTTTTCGAGCTTTAGCGGATCGGACAACTCTATTAAGTATGACAGATTGCTGTCAAGGA	6180

QY 6181 CCTAGTTCCTAGAGATAGACCGAAGCGAGGTGTGTGGCTGACGTTTCATGCCGTC 6240
| | | | |
Db 6181 CCTAGTTCCTAGAGATAGACCGAAGCGAGGTGTGTGGCTGACGTTTCATGCCGTC 6240
QY 6241 CAAGAGCCTGCCCCCTATTTCACCCGCAAGGCTAAAGAGATGGCCCGCTGGCAGCGGCA 6300
| | | | |
Db 6241 CAAGAGCCTGCCCCCTATTTCACCCGCAAGGCTAAAGAGATGGCCCGCTGGCAGCGGCA 6300
QY 6301 AGAAAAGAGCCCACTCCACCGGCAAGCATAGCTGTAGTCCCTCCACTCTCTTTGGT 6360
| | | | |
Db 6301 AGAAAAGAGCCCACTCCACCGGCAAGCATAGCTGTAGTCCCTCCACTCTCTTTGGT 6360
QY 6361 GGGGTATCCATGTCCCTCGATCAATTTTCGACGGAGAGACGGCCCGCAGGACGGTA 6420
| | | | |
Db 6361 GGGGTATCCATGTCCCTCGATCAATTTTCGACGGAGAGACGGCCCGCAGGACGGTA 6420
QY 6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCCGATCGTTTCCGACGGA 6480
| | | | |
Db 6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCCTATGTCTTTCCGATCGTTTCCGACGGA 6480
QY 6481 GAGATTGATGAGCTGAGCCGCGAGATTACTGAGTCCGAACCCGTCCTTTGGATCATTT 6540
| | | | |
Db 6481 GAGATTGATGAGCTGAGCCGCGAGATTACTGAGTCCGAACCCGTCCTTTGGATCATTT 6540
QY 6541 GAACCGGGGGAAGTGAATCAATTATATATGTCCTCCGATCAGCCGTAATCTTTCCACTACGC 6600
| | | | |
Db 6541 GAACCGGGGGAAGTGAATCAATTATATATGTCCTCCGATCAGCCGTAATCTTTCCACTACGC 6600
QY 6601 AAGCAGAGACGTAGACGACGACGAGACGAGACTGAATACTGACTAACCGGGGTAGGTGG 6660
| | | | |
Db 6601 AAGCAGAGACGTAGACGACGACGAGACGAGACTGAATACTGACTAACCGGGGTAGGTGG 6660
QY 6661 TACATATTTTGCACGGACACAGGCCCCCTGGGCACTTGCAAAAAGAGTCCGTTCTGCAGAAC 6720
| | | | |
Db 6661 TACATATTTTGCACGGACACAGGCCCCCTGGGCACTTGCAAAAAGAGTCCGTTCTGCAGAAC 6720
QY 6721 CAGCTTACAGAACCGACCTTGAGCGCAATGTCTCGAAAAGAAATTCATGCCCGGTGCTC 6780
| | | | |
Db 6721 CAGCTTACAGAACCGACCTTGAGCGCAATGTCTCGAAAAGAAATTCATGCCCGGTGCTC 6780
QY 6781 GACACGTCGAAGAGAACTCAAACTCAGGTTACAGATGATGCCCAAGGCAAGCCAAAC 6840
| | | | |
Db 6781 GACACGTCGAAGAGAACTCAAACTCAGGTTACAGATGATGCCCAAGGCAAGCCAAAC 6840
QY 6841 AAAAGTAGTACCACTCTCGTAAAGTAGAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
| | | | |
Db 6841 AAAAGTAGTACCACTCTCGTAAAGTAGAAATCAGAAAGCCATAACCACTGAGCGACTA 6900
QY 6901 CTGTCAAGACTACGACTGTATTAATCTGCGACAGATCAGCCAGAAATGCTATAAGATCACC 6960
| | | | |
Db 6901 CTGTCAAGACTACGACTGTATTAATCTGCGACAGATCAGCCAGAAATGCTATAAGATCACC 6960
QY 6961 TATCCGAACCAATTGTACTCCAGTAGCGTACGGGCAACTACTCCGATCCAAGTTGCT 7020
| | | | |
Db 6961 TATCCGAACCAATTGTACTCCAGTAGCGTACGGGCAACTACTCCGATCCAAGTTGCT 7020
QY 7021 GTAGCTGTCTGTAACTAATCTATCTGATGAGAACTATCCGACAGTAGCACTTATCAGATT 7080
| | | | |
Db 7021 GTAGCTGTCTGTAACTAATCTATCTGATGAGAACTATCCGACAGTAGCACTTATCAGATT 7080
QY 7081 ACTGACGAGTAGATGCTTACTTGATATGTGAGACGAGACAGTCCGATGCCCTGATACT 7140
| | | | |
Db 7081 ACTGACGAGTAGATGCTTACTTGATATGTGAGACGAGACAGTCCGATGCCCTGATACT 7140
QY 7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATAGAGCCCCG 7200
| | | | |
Db 7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATAGAGCCCCG 7200
QY 7201 AATATCCGAGTGGGTTCATCAGCGATGCAAGACGCTACAAAATGTCTCATTTGCC 7260
| | | | |
Db 7201 AATATCCGAGTGGGTTCATCAGCGATGCAAGACGCTACAAAATGTCTCATTTGCC 7260
QY 7261 GCAACTAAAAAATTTGCAACGTCAACGAGATGCGTGAACCTGCCAACACTGCAAGCG 7320
| | | | |

Db 7261 GCAACTAAAAAATTTGCAACGTCAACGAGATGCGTGAACCTGCCAACACTGCACTGACGG 7320
QY 7321 ACATTCATATGTCGAATGCTTTGAAAATATATGATGTAATGACGAGTATTGGAGAGTTTC 7380
| | | | |
Db 7321 ACATTCATATGTCGAATGCTTTGAAAATATATGATGTAATGACGAGTATTGGAGAGTTTC 7380
QY 7381 GCTCGAAGCCCAATTAGATTACCACTGAGTTGTGACCGCATATGTAGCTAGACTGAAA 7440
| | | | |
Db 7381 GCTCGAAGCCCAATTAGATTACCACTGAGTTGTGACCGCATATGTAGCTAGACTGAAA 7440
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| | | | |
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 VERSION AX128601.1
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 SOURCE
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 synthetic construct
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 other sequences; artificial sequences.

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 1 Renner, W.A. and Nieba, L.
 TITLE Method for creating divergent populations of nucleic acid molecules
 and proteins
 JOURNAL Patent: WO 0130989-A 1 03-MAY-2001;
 Cytos Biotechnology AG (CH); Renner, Wolfgang Andreas (CH);
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ACCESSION AX174827 GI:14598323
VERSION AX174827.1
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Hennecke, F. and Renner, W.A.
TITLE Activation of endogenous genes by genomic introduction of a replicon
JOURNAL Patent: WO 0142442-A 1 14-JUN-2001;
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ORIGIN

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QY	4081	GAACTGTTCCCAAGTTTCCGGATGACAAACCACATTCGGCCATTTACGCCCTTAGACGTA	4140
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Db	4141	ATTTCGATTAAAGTTTTCGGCATGGAATGCAAGCCGACTGTTTCTTAACAGAGCATC	4200
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Db	4561	GGCCCGCATTTGGCATAAGCCGGGTGCAGATTAAGAACTACAACCTGGCTTTCGGGTTTCCGCCG	4620
QY	4621	CAGGCACGGTACGACCCTGGTGTTCATCAACATTTGGAATAATAACAGAAACCACTTT	4680
Db	4621	CAGGCACGGTACGACCCTGGTGTTCATCAACATTTGGAATAATAACAGAAACCACTTT	4680
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Db	4861	GTTCTAAGCAATACAGAAATGTACTCTGATTTTCCGACAACCTAGACAACAGCGGTACACGG	4920
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RESULT 6
CQ790429 13068 bp DNA linear PAT 29-MAR-2004

LOCUS CQ790429 Sequence 2 from Patent WO2004018506.

DEFINITION CQ790429 CQ790429.1 GI:45823471

ACCESSION CQ790429.1

VERSION CQ790429.1

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Ivanova, L., Renner, W.A. and Saudan, P.
TITLE Inducible alphavirus/orip based gene expression system
JOURNAL Patent: WO 2004018506-A 2 04-MAR-2004;
Cytos Biotechnology AG (CH)
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ORIGIN

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REFERENCE   1
AUTHORS     Ivanova,L., Renner,W.A. and Saudan,P.
TITLE       Inducible alphaviral/orip based gene expression system
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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
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QY      1433 GAACTATCTATCATCAGGCTATGAAGCGGTGCGGACCTGTACTGATTGGCTTGACA 1492
      |||||||
Db      1409 GAACTATCTATCATCAGGCTATGAAGCGGTGCGGACCTGTACTGATTGGCTTGACA 1468
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QY      1493 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTTCGTACCCCTGCGTACACACCACTGGG 1552
      |||||||
Db      1469 CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTTCGTACCCCTGCGTACACACCACTGGG 1528

QY      1553 CCGACGAGAAAGTCTTGAAAGCGGCTAACATCGGACTTTGACAGCACAAAGCTGAGTGAAG 1612
      |||||||
Db      1529 CCGACGAGAAAGTCTTGAAAGCGGCTAACATCGGACTTTGACAGCACAAAGCTGAGTGAAG 1588

QY      1613 GTAGGACAGGAAATGTGATAATGAGGAAGAGGTTGAAGCCCGGGTCGGGGTTT 1672
      |||||||
Db      1589 GTAGGACAGGAAATGTGATAATGAGGAAGAGGTTGAAGCCCGGGTCGGGGTTT 1648

QY      1673 ATTTCTCCGTAGATCGACACTTATCCAGAAACAGAGCCAGCTTGACAGAGTGGCATC 1732
      |||||||
Db      1649 ATTTCTCCGTAGATCGACACTTATCCAGAAACAGAGCCAGCTTGACAGAGTGGCATC 1708

QY      1733 TTCCATCGGTGTTCCACTTGAATGGAAGCAGTCTGTACTTGCCCGCTGTATACAGTGG 1792
      |||||||
Db      1709 TTCCATCGGTGTTCCACTTGAATGGAAGCAGTCTGTACTTGCCCGCTGTATACAGTGG 1768

QY      1793 TGAATTGCGAAGGCTACGTAGTGAAGAAATCACCATAGTCCCGGATCACGGGAGAA 1852
      |||||||
Db      1769 TGAATTGCGAAGGCTACGTAGTGAAGAAATCACCATAGTCCCGGATCACGGGAGAA 1828

QY      1853 CCGTGGATACGCGGTTACACACAATAGCGAGGCTTCTTGCTATGCAAAAGTTACTGACA 1912
      |||||||
Db      1829 CCGTGGATACGCGGTTACACACAATAGCGAGGCTTCTTGCTATGCAAAAGTTACTGACA 1888

QY      1913 CAGTAAAAAGAGAACGGGTATCGTTCCTGTGTGCACTGATCCCGGCCACCATATGCG 1972
      |||||||
Db      1889 CAGTAAAAAGAGAACGGGTATCGTTCCTGTGTGCACTGATCCCGGCCACCATATGCG 1948

QY      1973 ATCAGATGACTGTATTAATGGCCACGATATATCACTGACGATGCACAAAACTTCTGG 2032
      |||||||
Db      1949 ATCAGATGACTGTATTAATGGCCACGATATATCACTGACGATGCACAAAACTTCTGG 2008

QY      2033 TTGGGCTCAACCAAGCAATTGTCACTTAACGGTAGACTTAACAGAACCAACCAACCATGC 2092
      |||||||
Db      2009 TTGGGCTCAACCAAGCAATTGTCACTTAACGGTAGACTTAACAGAACCAACCAACCATGC 2068

QY      2093 AAAATTACCTTCTGCGCATCAATGACACAAGGTTTACGAAATGGGCTAAGAGCGCAAG 2152
      |||||||
Db      2069 AAAATTACCTTCTGCGCATCAATGACACAAGGTTTACGAAATGGGCTAAGAGCGCAAG 2128

QY      2153 ATGATCTTGATAACGAGAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGTGTCT 2212
      |||||||
Db      2129 ATGATCTTGATAACGAGAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGTGTCT 2188

QY      2213 TGTGGCGTTTTCGCACTAAGAAAGTACATTCGTTTATCGCCCACTGGAACGACAGCT 2272
      |||||||
Db      2189 TGTGGCGTTTTCGCACTAAGAAAGTACATTCGTTTATCGCCCACTGGAACGACAGCT 2248

QY      2273 GCGTAAAAAGTCCAGACCTCTTTAGCGCTTTTCCAGTCTGCTCCGTATGACGACCTCTT 2332
      |||||||
Db      2249 GCGTAAAAAGTCCAGACCTCTTTAGCGCTTTTCCAGTCTGCTCCGTATGACGACCTCTT 2308

QY      2333 TGCCCATGTCGCTGAGGCGAATTTGAACTGGCATTTGCAACCAAGAAGAGGAAAAAC 2392
      |||||||
Db      2309 TGCCCATGTCGCTGAGGCGAATTTGAACTGGCATTTGCAACCAAGAAGAGGAAAAAC 2368

QY      2393 TGTGTCAGGTCTCGGAGGAATTAATCATGGAAGGCCAAGGCTCTTTGAGGATGCTCAGG 2452
      |||||||
Db      2369 TGTGTCAGGTCTCGGAGGAATTAATCATGGAAGGCCAAGGCTCTTTGAGGATGCTCAGG 2428

QY      2453 AGGAAGCCAGAGCGGAGAAAGCTCCGAGAGCACTTCCACATTAAGTGAGAGCAAAAGGCA 2512
      |||||||
Db      2429 AGGAAGCCAGAGCGGAGAAAGCTCCGAGAGCACTTCCACATTAAGTGAGAGCAAAAGGCA 2488

QY      2513 TCGAGGCAAGCCGAGAAAGTGTCTGCGAAGTGAAGGGCTCCAGGCGGACATCGAGAGAG 2572
      |||||||
Db      2489 TCGAGGCAAGCCGAGAAAGTGTCTGCGAAGTGAAGGGCTCCAGGCGGACATCGAGAGAG 2548

QY      2573 CATTAAGTTGAACCCCGCGGTCAAGTAAGATAATACCTCAAGCAATGACCGTATGA 2632
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Db 2549 CATTAGTTGAAACCCCGCGGTCACGTAAGATAATACCTCAAGCAAAATGACCGTATGA 2608
QY 2633 TCGGACAGTATATCGTTGTCGCGCAAACTCTGTGCTGAAGAAATGCCAAATCGCACCAG 2692
Db 2609 TCGGACAGTATATCGTTGTCGCGCAAACTCTGTGCTGAAGAAATGCCAAATCGCACCAG 2668
QY 2693 CGCACCCCGCTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAGGAAGGTACG 2752
Db 2669 CGCACCCCGCTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAGGAAGGTACG 2728
QY 2753 CGGTGCAACCATACGACGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAG 2812
Db 2729 CGGTGCAACCATACGACGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAG 2788
QY 2813 AATTCTAGCACTGAGTGAGAGCGCCACGTTAGTGTTACAAACGAAAGAGAGTTTGTGAACC 2872
Db 2789 AATTCTAGCACTGAGTGAGAGCGCCACGTTAGTGTTACAAACGAAAGAGAGTTTGTGAACC 2848
QY 2873 GCAAACTATACCACTTGGCCATGCAATGCCCCCGCCAAAGATAAGAGAGAGCAGTACA 2932
Db 2849 GCAAACTATACCACTTGGCCATGCAATGCCCCCGCCAAAGATAAGAGAGAGCAGTACA 2908
QY 2933 AGGTTACAAAGGCAGAGCTTGCAAAACAGAGTACGTGTTGACGTGCAACAAGACGTT 2992
Db 2909 AGGTTACAAAGGCAGAGCTTGCAAAACAGAGTACGTGTTGACGTGCAACAAGACGTT 2968
QY 2993 GCGTTAAGAGGAAGAACCTCAGGTCGTGCTCTCTCGGAGAACTGACCAACCTCCCT 3052
Db 2969 GCGTTAAGAGGAAGAACCTCAGGTCGTGCTCTCTCGGAGAACTGACCAACCTCCCT 3028
QY 3053 ATCATGAGTAGCTCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTAACAAGTCGAAA 3112
Db 3029 ATCATGAGTAGCTCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTAACAAGTCGAAA 3088
QY 3113 CAATAGAGTAGTAGGCACACCGGGTCGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3172
Db 3089 CAATAGAGTAGTAGGCACACCGGGTCGGCAAGTCAGCTATTATCAAGTCAACTGTCA 3148
QY 3173 CGGCACGAGATCTTGTACCAGCGGAAGAAAGAAATTTGCGGAAATTGAGCCGACG 3232
Db 3149 CGGCACGAGATCTTGTACCAGCGGAAGAAAGAAATTTGCGGAAATTGAGCCGACG 3208
QY 3233 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTGCGTTATGCTCAACG 3292
Db 3209 TGCTAAGACTGAGGGGTATGCAGATTACGTCGAAGACAGTAGATTGCGTTATGCTCAACG 3268
QY 3293 GATGCCACAAGCCGTAGAAGTGTGTAAGTGAAGAGCGTTCCGCTGCCACGACGAGAG 3352
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QY 3353 CACTACTGCTTGATTGCTATCGTCAAGCCCCCGCAAGAAGTAGTACTATGCGGAGACC 3412
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Db 3389 CCATGCAATGCGGATTCTTCAACATGATGCAACTAAAGGTACATTCAATCAACCTGAAA 3448
QY 3473 AAGACATATGCAACCAAGACATTCTCAAGTATATCTCCGGCGTTGACACAGCCAGTTA 3532
Db 3449 AAGACATATGCAACCAAGACATTCTCAAGTATATCTCCGGCGTTGACACAGCCAGTTA 3508
QY 3533 CAGCTATTGTATGCACACTGCATTACGATGGAAGATGAAAAACACGAAACCCGTGCAAGA 3592
Db 3509 CAGCTATTGTATGCACACTGCATTACGATGGAAGATGAAAAACACGAAACCCGTGCAAGA 3568
QY 3593 AGAACATTGAATCGATATTACAGGGGCCAAGCCGAAGCCAGGGGATATCATCTCTGA 3652
Db 3569 AGAACATTGAATCGATATTACAGGGGCCAAGCCGAAGCCAGGGGATATCATCTCTGA 3628
QY 3653 CATGTTCCGGGGTGGGTTAAGCAATTGCAAAATGCACTATCCCGGACATGAAGTATGA 3712

Db 3629 CATGTTCCGGGGTGGGTTAAGCAATTGCAAAATGCAATCGACTATCCCGGACATGAAGTATGA 3688
QY 3713 CAGCCGGGCTTCACAAGGCTTAACGAGAAAAAGAGTGTATGCCGTCGCCAAAAAGTCA 3772
Db 3689 CAGCCGGGCTTCACAAGGCTTAACGAGAAAAAGAGTGTATGCCGTCGCCAAAAAGTCA 3748
QY 3773 ATGAAAACCACTGTACGCGGATCAGATGAGAGCATGTGAACGTGTGCTCACCCGCACTG 3832
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QY 3833 AGGACAGGCTAGTGTGAAAAACCTTGCAAGGCGACCCCATGATTAAGCAGCCCACTAACA 3892
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Db 3929 TTGCTGCAATAAACAGCCCCCACTCCCGGTGCCAATCCGTTACGTGCAAGACCAAGCTTT 3988
QY 4013 GCTGGCGGAAGCATTTGGAACCGATACAGCACGCGCGGTATGCTTACCGGTGCCC 4072
Db 3989 GCTGGCGGAAGCATTTGGAACCGATACAGCACGCGCGGTATGCTTACCGGTGCCC 4048
QY 4073 AGTGAGCGAACTGTTCCCAAGTTTCCGGATGACAAACCAACTTCCGCAATTTACGCCCT 4132
Db 4049 AGTGAGCGAACTGTTCCCAAGTTTCCGGATGACAAACCAACTTCCGCAATTTACGCCCT 4108
QY 4133 TAGACGTAATTTGCATTAAGTTTTCGCGATGAGACTTGACAAAGCGGACTGTTTCTAAAC 4192
Db 4109 TAGACGTAATTTGCATTAAGTTTTCGCGATGAGACTTGACAAAGCGGACTGTTTCTAAAC 4168
QY 4193 AGAGCATCCCACTAACGTACCATCCCGCGGATTCAAGCGAGGCCGGTAGCTCATTTGGACA 4252
Db 4169 AGAGCATCCCACTAACGTACCATCCCGCGGATTCAAGCGAGGCCGGTAGCTCATTTGGACA 4228
QY 4253 ACAGCCCAAGAAACCCGCAAGTATGGTACGATCAGCCCATTTGCCGGAACCTCTCCGTA 4312
Db 4229 ACAGCCCAAGAAACCCGCAAGTATGGTACGATCAGCCCATTTGCCGGAACCTCTCCGTA 4288
QY 4313 GATTTCCGGTGTCCAGCTAGCTGGGAAGGCAACAACCTTGATTGCAAGCGGAGAA 4372
Db 4289 GATTTCCGGTGTCCAGCTAGCTGGGAAGGCAACAACCTTGATTGCAAGCGGAGAA 4348
QY 4373 CCAGAGTTATCTCTGCACAGCATTAACCTGTCGCCGCTGAACCGCAATCTTCTCACGCCCT 4432
Db 4349 CCAGAGTTATCTCTGCACAGCATTAACCTGTCGCCGCTGAACCGCAATCTTCTCACGCCCT 4408
QY 4433 TAGTCCCGGAGTACAAGAGAAAGCAACCCGCGCCGCTCAAAAAAATTCTTGAAACCAAGTTCA 4492
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QY 4553 AATGATCGCCCCGATTGGCATAGCCGGTGCAATGAAGACTCAACCTGACTTTCGGGT 4612
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QY 4613 TTCCGCGGACGACCGGTACGACCTGTGTTCATCAACATTGGAACCTAAATACAGAAACC 4672
Db 4589 TTCCGCGGACGACCGGTACGACCTGTGTTCATCAACATTGGAACCTAAATACAGAAACC 4648
QY 4673 ACCACTTTACAGAGTCCGAAGACCATGCGGCACTTAAAAAACCTTTTCGCGTTCCGCCCC 4732
Db 4649 ACCACTTTACAGAGTCCGAAGACCATGCGGCACTTAAAAAACCTTTTCGCGTTCCGCCCC 4708
QY 4733 TGAATTGTTAAACTCAGAGAGGACCTCTGTGTGAAGTCTTATGGCTACGCCGACCGCA 4792
Db 4709 TGAATTGTTAAACTCAGAGAGGACCTCTGTGTGAAGTCTTATGGCTACGCCGACCGCA 4768

QY	4793	ACAGTGAAGGACGTAGTCAACCGCTCTTGCCAGAAAAGTTGTGACGGGTGTCTGCAGCGAGAC	4852
Db	4769	ACAGTGAGGACGTAGTCAACCGCTCTTGCCAGAAAAGTTGTGACGGGTGTCTGCAGCGAGAC	4828
QY	4853	CAGATTGTGTCTCAAGCAATACAGAAATGTACTCTGATTTTCCGACCACTAGACAAACGCC	4912
Db	4829	CAGATTGTGTCTCAAGCAATACAGAAATGTACTCTGATTTTCCGACCACTAGACAAACGCC	4888
QY	4913	GTACACGGCAATTCAACCCCGCACCATCTGAATTGCGTGATTTGTCCTGTATGAGGTA	4972
Db	4889	GTACACGGCAATTCAACCCCGCACCATCTGAATTGCGTGATTTGTCCTGTATGAGGTA	4948
QY	4973	CAAGAGATGAGTTGAGCGCGCGCGCTCATACCGCACCAAAAGGAGAATATTGCTGACT	5032
Db	4949	CAAGAGATGAGTTGAGCGCGCGCGCTCATACCGCACCAAAAGGAGAATATTGCTGACT	5008
QY	5033	GTCAAGAGGAGACAGTTGTCAACGCAGCCCAATCCGCTGGGTAGACCAGCGGAAGAGTCT	5092
Db	5009	GTCAAGAGGAGACAGTTGTCAACGCAGCCCAATCCGCTGGGTAGACCAGCGGAAGAGTCT	5068
QY	5093	GCCGTGCCATCTATAACGTTGGCCGACCAAGTTTACCGATTACGCCAGGAGACAGCA	5152
Db	5069	GCCGTGCCATCTATAACGTTGGCCGACCAAGTTTACCGATTACGCCAGGAGACAGCA	5128
QY	5153	CCGCAAGAATGACTGTGTGCTTAGAAAAAGAAAGTGATCCACGGCTCGCCCTGATTTCC	5212
Db	5129	CCGCAAGAATGACTGTGTGCTTAGAAAAAGAAAGTGATCCACGGCTCGCCCTGATTTCC	5188
QY	5213	GGAAGCACCCAGAAAGCAGAAAGCCTTGAATTTGTACAAAACGCTTACCATGCAGTGGCAG	5272
Db	5189	GGAAGCACCCAGAAAGCAGAAAGCCTTGAATTTGTACAAAACGCTTACCATGCAGTGGCAG	5248
QY	5273	ACTTAGTAATGAACATTAACATCAAGTCTGTGCGCATTCACCTGCTATCTACAGGCATTT	5332
Db	5249	ACTTAGTAATGAACATTAACATCAAGTCTGTGCGCATTCACCTGCTATCTACAGGCATTT	5308
QY	5333	ACGCAGCCCGAAAAAGACCGGCTTGAAGTATCACTTACTGTTGACAAACCGCGCTAGACA	5392
Db	5309	ACGCAGCCCGAAAAAGACCGGCTTGAAGTATCACTTACTGTTGACAAACCGCGCTAGACA	5368
QY	5393	GAACTGACGCGGACGTAACCATCTATTGCTTGATTAAGAAAGTGAAAGAAAGATTCGACG	5452
Db	5369	GAACTGACGCGGACGTAACCATCTATTGCTTGATTAAGAAAGTGAAAGAAAGATTCGACG	5428
QY	5453	CGGCACTCCAACTTAAGAGGTCTGTAAACAGAGCTGAAGGATGAAGATATGAGATCGACG	5512
Db	5429	CGGCACTCCAACTTAAGAGGTCTGTAAACAGAGCTGAAGGATGAAGATATGAGATCGACG	5488
QY	5513	ATGAGTTAGTATGATTCAATCCAGACAGTTGCTTGAAGGAAAGAAAGGATTCACTTA	5572
Db	5489	ATGAGTTAGTATGATTCAATCCAGACAGTTGCTTGAAGGAAAGAAAGGATTCACTTA	5548
QY	5573	CAAAAAGAAAAATGTATTCGTACTTTCGAAGGACACCAATTCATCAAGCAGCAAAAAGACA	5632
Db	5549	CAAAAAGAAAAATGTATTCGTACTTTCGAAGGACACCAATTCATCAAGCAGCAAAAAGACA	5608
QY	5633	TGGCGAGATAAAGTCTGTTCCTTAATGACCAGAAAGTAATGAACAACTGTGTGCTT	5692
Db	5609	TGGCGAGATAAAGTCTGTTCCTTAATGACCAGAAAGTAATGAACAACTGTGTGCTT	5668
QY	5693	ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAAGTCCCGGTGCACCAATACCCGT	5752
Db	5669	ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAAGTCCCGGTGCACCAATACCCGT	5728
QY	5753	CGTCTAGCCCCGCCAAAAAGTTCGCCGTGCTTTCGATGTATGCCATGACGCCAGAAAAGGG	5812
Db	5729	CGTCTAGCCCCGCCAAAAAGTTCGCCGTGCTTTCGATGTATGCCATGACGCCAGAAAAGGG	5788
QY	5813	TCCACAGACTTAGAAGCAATTAAGTCAAAAGAGTTACAGTATGCTCTCCACCCCCCTTC	5872
Db	5789	TCCACAGACTTAGAAGCAATTAAGTCAAAAGAGTTACAGTATGCTCTCCACCCCCCTTC	5848

QY	5873	CTAAGCACAAATTAAGAAATGTTTCAGAAAGGTTCAGTGCACGAAAGTAGTCTGTGTTAATC	5932
Db	5849	CTAAGCACAAATTAAGAAATGTTTCAGAAAGGTTCAGTGCACGAAAGTAGTCTGTGTTAATC	5908
QY	5933	CGCACACTCCCGCAATTCGTTCCCGCCGTAAGTACATAGAAGTCCAGAAACAGCCTACCG	5992
Db	5909	CGCACACTCCCGCAATTCGTTCCCGCCGTAAGTACATAGAAGTCCAGAAACAGCCTACCG	5968
QY	5993	CTCTCTCTGCACAGGCCGAGAGAGGCCCCCGAAGTTGTAGCGACACCGTCAACCATTTACAG	6052
Db	5969	CTCTCTCTGCACAGGCCGAGAGAGGCCCCCGAAGTTGTAGCGACACCGTCAACCATTTACAG	6028
QY	6053	CTGATAACACCTCGCTTGTATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG	6112
Db	6029	CTGATAACACCTCGCTTGTATGTCACAGACATCTCACTGGATATGGATGACAGTAGCGAAG	6088
QY	6113	GCTCACTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGACAGTTGGT	6172
Db	6089	GCTCACTTTTTCGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGACAGTTGGT	6148
QY	6173	CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGAGGAGGTGGTGGTGAAGTTTC	6232
Db	6149	CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAGGAGGAGGTGGTGGTGAAGTTTC	6208
QY	6233	ATGCCGTCCAAGAGCCTGCCCCCTATTCCACCGCCAAAGGCTAAAGAAGATGGCCCCCTGG	6292
Db	6209	ATGCCGTCCAAGAGCCTGCCCCCTATTCCACCGCCAAAGGCTAAAGAAGATGGCCCCCTGG	6268
QY	6293	CAGCGGCAAGAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT	6352
Db	6269	CAGCGGCAAGAAAGAGCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCT	6328
QY	6353	CTTTTGGTGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCCGACAG	6412
Db	6329	CTTTTGGTGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCCGACAG	6388
QY	6413	CAGCGGTACAAACCCCTGGCAACAGGCCCCCAGCGATGTGCTTATGTCCTTCGGATCGTTT	6472
Db	6389	CAGCGGTACAAACCCCTGGCAACAGGCCCCCAGCGATGTGCTTATGTCCTTCGGATCGTTT	6448
QY	6473	CCGACGGAGAGATGATGAGCTGAGCCGCGAGATTACTGAGTCCGAACCCGTCCTGTTG	6532
Db	6449	CCGACGGAGAGATGATGAGCTGAGCCGCGAGATTACTGAGTCCGAACCCGTCCTGTTG	6508
QY	6533	GATCATTTGAAACGGGGCGAAGTGAACTCAATTATCGTCCCGATCAGCCGTAATCTTTTC	6592
Db	6509	GATCATTTGAAACGGGGCGAAGTGAACTCAATTATCGTCCCGATCAGCCGTAATCTTTTC	6568
QY	6593	CACTACGCAAGCAGAGACGTAGACCGCAGAGCAGGAGGACTGAATCTGACTAAACCGGGG	6652
Db	6569	CTCTACGCAAGCAGAGACGTAGACCGCAGAGCAGGAGGACTGAATCTGACTAAACCGGGG	6628
QY	6653	TAGTGGGTACATATTTTCGACCGGACACAGGCCCTGGGCACTTGCAGAAAGAGTCCGTTT	6712
Db	6629	TAGTGGGTACATATTTTCGACCGGACACAGGCCCTGGGCACTTGCAGAAAGAGTCCGTTT	6688
QY	6713	TGCAGAACCAAGCTTACAGAAACCGACCTTGGAGCGCAATGTCCTGGAAGAAATTCATGCC	6772
Db	6689	TGCAGAACCAAGCTTACAGAAACCGACCTTGGAGCGCAATGTCCTGGAAGAAATTCATGCC	6748
QY	6773	CGGTGCTCGACAGTCGAAAGAGAACTCAAACTCAGGTACCAAGTAGTCCCAACCG	6832
Db	6749	CGGTGCTCGACAGTCGAAAGAGAACTCAAACTCAGGTACCAAGTAGTCCCAACCG	6808
QY	6833	AAGCCAACAAAGTAGGTACCAAGTCTCGTAAAGTAGAAATCAGAAAGCCATAACCACTG	6892
Db	6809	AAGCCAACAAAGTAGGTACCAAGTCTCGTAAAGTAGAAATCAGAAAGCCATAACCACTG	6868
QY	6893	AGCGACTACTGTCAAGACTACGACTGTGTAATACTTGCCACAGATCAGCCAGAAATGCTATA	6952
Db	6869	AGCGACTACTGTCAAGACTACGACTGTGTAATACTTGCCACAGATCAGCCAGAAATGCTATA	6928
QY	6953	AGATCACTATCCGAAACCAATGTACTCCAGTAGCCGTACCGGCGAACTACTCCGATCCAC	7012

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Db 6929 AGATCACCTATCCGAAACCATTTGACTCCAGTAGCGTACC GGCGAACTACTCCGATCCAC 6988
Qy 7013 AGTTCGCTGTAGCTGTCTGTAACTATCTGCTGAGAACTATCCGACAGTAGCATCTT 7072
Db 6989 AGTTCGCTGTAGCTGTCTGTAACTATCTGCTGAGAACTATCCGACAGTAGCATCTT 7048
Qy 7073 ATCAGATTACTGACGAGTAGCATGCTTACTTGATATGTAGACGAGACAGTCCGATGCC 7132
Db 7049 ATCAGATTACTGACGAGTAGCATGCTTACTTGATATGTAGACGAGACAGTCCGATGCC 7108
Qy 7133 TGGATATCTGCAACCTTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATA 7192
Db 7109 TGGATATCTGCAACCTTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATA 7168
Qy 7193 GAGCCCCGAATATCCGAGTGCAGTCCGCTTCATCAGCGATGCAGAACACGCTACAAATGTGC 7252
Db 7169 GAGCCCCGAATATCCGAGTGCAGTCCGCTTCATCAGCGATGCAGAACACGCTACAAATGTGC 7228
Qy 7253 TCATTGCCGCAACTAAAGAAATTGCAACGTCACGAGATGCGTGAACCTGCCAACACTGG 7312
Db 7229 TCATTGCCGCAACTAAAGAAATTGCAACGTCACGAGATGCGTGAACCTGCCAACACTGG 7288
Qy 7313 ACTCAGCGACATTCATGTCTGATGCTTTCGAAAAATATGCATGTATGACGAGTATTGGG 7372
Db 7289 ACTCAGCGACATTCATGTCTGATGCTTTCGAAAAATATGCATGTATGACGAGTATTGGG 7348
Qy 7373 AGGAGTTCGCTCGGAAGCCAAATTAGATTACCACTGAGTTGTCCACCGCATATGTAGCTA 7432
Db 7349 AGGAGTTCGCTCGGAAGCCAAATTAGATTACCACTGAGTTGTCCACCGCATATGTAGCTA 7408
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Db 7529 GCACGAAACACACAGAAAGAACCCGAAAGTACAACTGATACAGCCGCGAGAACCCCTGG 7588
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Qy 7793 AAGACGACGCTATGGCGTTAACCCGCTCTGATGATCTTGAGAGACCTGGGTGATCAAC 7852
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Qy 8033 GATGTGACGCTTCAATTGGCGACGACACATCATGAGTAGTATCTGACAAAGAA 8092
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Db 8009 GATGTGACGCTTCAATTGGCGACGACACACATCATGAGTAGTATCTGACAAAGAA 8068
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LOCUS CQ790449
DEFINITION Sequence 22 from Patent WO2004018506.
ACCESSION CQ790449
VERSION CQ790449.1 GI:45823491
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SOURCE
ORGANISM
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1 Ivanova, L., Renner, W.A. and Saudan, P.
AUTHORS Inducible alpha viral/orip based gene expression system
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JOURNAL Cytos Biotechnology AG (CH)
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RESULT 9
LOCUS AR282858 9951 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from patent US 6524792.
ACCESSION AR282858
VERSION AR282858.1 GI:29719660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 9951)
AUTHORS Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.
TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property
JOURNAL Patent: US 6524792-A 3 25-FEB-2003;
FEATURES
source location/Qualifiers
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ORIGIN
Query Match 89.4%; Score 7637.4; DB 6; Length 9951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 1 ATTGACGCGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCACTACCATCACAA 60
QY 953 TGGAGAGCCAGTAGTAACGTAGACGTAGACCCCCAGAGTCCGTTGTCGTCAACTGC 1012
Db 61 TGGAGAGCCAGTAGTAACGTAGACGTAGACCCCCAGAGTCCGTTGTCGTCAACTGC 120
QY 1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTACACAGCAGAGTCACTCCAAATGACCATGCTA 1072
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QY 1073 ATGCCAGACATTTTCGCATCTGGCCAGTAACTAATCGAGCTGGAGGTTCTTACCACAG 1132
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QY 1193 ATTGTCTGCCCATGCGTAGTCCGAGAAAGCCCGACCGCATGATGAATAGCCAGTA 1252
Db 301 ATTGTCTGCCCATGCGTAGTCCGAGAAAGCCCGACCGCATGATGAATAGCCAGTA 360
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QY 1313 TCCGACCGTACTTGATACGCCCGGATGTGAACAACCATCGCTTCTTTCACAACGATG 1372
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QY 2333 TGCCCATGTGCTGAGGCAAAATTGAAACTGGCATTGCAACCAAGAAGAGAAAAC 2392
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KEYWORDS	SYNTHETIC CONSTRUCT
SOURCE	synthetic construct
ORGANISM	synthetic construct
	other sequences; artificial sequences.

REFERENCE	AUTHORS	TITLE	JOURNAL
1	Renner, W.A. and Nieba, L.	Method for creating divergent populations of nucleic acid molecules and proteins	Patent: WO 0130989-A 2 03-MAY-2001;

Cytos Biotechnology AG (CH) ; Renner, Wolfgang Andreas (CH) ;
Nieba, Lars (CH)

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ORIGIN

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AR282859
LOCUS AR282859 10524 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 4 from patent US 6524792.
ACCESSION AR282859
VERSION AR282859.1 GI:29719661
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10524)
AUTHORS Renner, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.
TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property
JOURNAL Patent: US 6524792-A 4 25-FEB-2003;
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ORIGIN
Query Match 89.4%; Score 7637.4; DB 6; Length 10524;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY	1013	AAAAAGCTTCCCGCAATTGAGGTAG	TAGACAGAGGTCACTCCAATGACCA	1072
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QY	1133	CGACGATCTTGACATAGCGACGCGC	ACCGGCTCGTAGAATGTTTCCGAGC	1192
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QY	1193	ATTGTGTCGCCCCATGCGTAGTCC	AGAAGACCCGCGCATGATGAATACG	1252
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Db	1921	AATTCTAGCACTGAGTGAAGAGCGCCACGTTAGTGTACAACGAAAGAGAGTTGTGAACC	1980
QY	2873	GCAAACTATACCATGTCATGCGCCCGCCCAAGAAATACAGAAAGAGAGCAGTACA	2932
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DEFINITION Sequence 5 from patent US 6524792.
ACCESSION AR282860
VERSION AR282860.1 GI:29719662
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
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AUTHORS Renner, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.
TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property
JOURNAL Patent: US 6524792-A 5 25-FEB-2003;
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source location/Qualifiers
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ORIGIN

Query Match 89.4%; Score 7637.4; DB 6; Length 11927;
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RESULT 13
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DEFINITION Sequence 1 from patent US 6197502.
ACCESSION ARI37241
VERSION ARI37241.1 GI:14478750
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13905)
AUTHORS Renner, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.
TITLE Expression cloning processes for the discovery characterization,
and isolation of genes encoding polypeptides with a predetermined
property
Patent: US 6197502-A 1 06-MAR-2001;
Location/Qualifiers
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/organism="unknown"
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ORIGIN

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Query Match	Best Local Similarity	Matches 7641, Conservative	89.4%; Score 7637.4; DB 6; Length 13905;	Pred. No. 0;	Mismatches 0;	Indels 6;	Gaps 0;
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QY	953	TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTGTGCTGCACTGC	1012				
Db	61	TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTGTGCTGCACTGC	120				
QY	1013	AAAAAAGCTTCCCGCAATTTAGGTAGTAGACACAGCAGGTCACTCCAAATGACCATGCTA	1072				
Db	121	AAAAAAGCTTCCCGCAATTTAGGTAGTAGACACAGCAGGTCACTCCAAATGACCATGCTA	180				
QY	1073	ATGCCAGAGCATTTCCGACTCTGGCCAGTAACCTAATCGAGCTGGAGGTTCTTACCACAG	1132				

Db	181	ATGCCAGAGCATTTTCGCATCTGGCCAGTAACTAATCGAGCTGGAGGTTCCATCCACAG	240
QY	1133	CGACGATCTTGGACATATGAGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC	1192
Db	241	CGACGATCTTGGACATAGGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACCAGTATC	300
QY	1193	ATTGTGTCTGCCCATGCGTAGTCCAGAAGACCCGGACCCGCATGATGAATAACCCAGTA	1252
Db	301	ATTGTGTCTGCCCATGCGTAGTCCAGAAGACCCGGACCCGCATGATGAATAACCCAGTA	360
QY	1253	AACTGGCGGAAAAAGCGTGCAAGATTACAACAGAACTTGATGAGAAGATTAAAGATC	1312
Db	361	AACTGGCGGAAAAAGCGTGCAAGATTACAACAGAACTTGATGAGAAGATTAAAGATC	420
QY	1313	TCCGGAACCGTACTGTATACGCCCGGATGCTGAAACACCATCGCTCTGCTTTCAACGATG	1372
Db	421	TCCGGAACCGTACTGTATACGCCCGGATGCTGAAACACCATCGCTCTGCTTTCAACGATG	480
QY	1373	TTAAGTGCACATGCGTGCAGATATATCCGTCATGACAGACGTATATCAACGCTCCCG	1432
Db	481	TTAAGTGCACATGCGTGCAGATATATCCGTCATGACAGACGTATATCAACGCTCCCG	540
QY	1433	GAACTATCTATCATCAGGCTATGAAAGCGTGCAGACCCCTGTACTGTGATTGGCTTCACA	1492
Db	541	GAACTATCTATCATCAGGCTATGAAAGCGTGCAGACCCCTGTACTGTGATTGGCTTCACA	600
QY	1493	CCACCCAGTTCATGTTCTCGGCTATGCGCAGGTTGTAACCTGCGTACCAACCAACTGGG	1552
Db	601	CCACCCAGTTCATGTTCTCGGCTATGCGCAGGTTGTAACCTGCGTACCAACCAACTGGG	660
QY	1553	CCGACGAGAAAGTCCTTGAAGCGCGTAACATCCGACTTTGCAGACAAAGCTGAGTGAAG	1612
Db	661	CCGACGAGAAAGTCCTTGAAGCGCGTAACATCCGACTTTGCAGACAAAGCTGAGTGAAG	720
QY	1613	GTAGACAGGAAAAATTGTCGATATAGAGGAAGAGAGTGAAGCCCGGGTTCGGGGTTT	1672
Db	721	GTAGACAGGAAAAATTGTCGATATAGAGGAAGAGAGTGAAGCCCGGGTTCGGGGTTT	780
QY	1673	ATTTCTCCGTAGATCGACACTTTATCCAGAACAGAGCCAGCTTGACAGCTGGCATC	1732
Db	781	ATTTCTCCGTAGATCGACACTTTATCCAGAACAGAGCCAGCTTGACAGCTGGCATC	840
QY	1733	TTCCATCGGTGCCACTTGAATGGAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG	1792
Db	841	TTCCATCGGTGCCACTTGAATGGAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG	900
QY	1793	TGAGTTGCCAAGGCTACGTAGTGAAGAAAAATCACATCAGTCCCGGATCACGGGAGAAA	1852
Db	901	TGAGTTGCCAAGGCTACGTAGTGAAGAAAAATCACATCAGTCCCGGATCACGGGAGAAA	960
QY	1853	CCGTGGATACCGCGTTACACACAATAGCGAGGCTTCTTGCTATGCAAGTTACTGACA	1912
Db	961	CCGTGGATACCGCGTTACACACAATAGCGAGGCTTCTTGCTATGCAAGTTACTGACA	1020
QY	1913	CAGTAAAAAGAGAACGGGTATCGTTCCCTGTGTGACAGTACATCCCGGCCACCATATGG	1972
Db	1021	CAGTAAAAAGAGAACGGGTATCGTTCCCTGTGTGACAGTACATCCCGGCCACCATATGG	1080
QY	1973	ATCAGATGACTGTGTAATATGCGCACCGATATATCACTGACGATGCACAAAACTTCTGG	2032
Db	1081	ATCAGATGACTGTGTAATATGCGCACCGATATATCACTGACGATGCACAAAACTTCTGG	1140
QY	2033	TTGGGCTCAACCAAGCAATTTGTCATTAAACGGTAGGACTAACAGAAACCAACCATATGC	2092
Db	1141	TTGGGCTCAACCAAGCAATTTGTCATTAAACGGTAGGACTAACAGAAACCAACCATATGC	1200
QY	2093	AAAATTACCTTCTGCCGATCATAGCACAAAGGTTCAACAATGGGCTAAGAGCGCAAGG	2152
Db	1201	AAAATTACCTTCTGCCGATCATAGCACAAAGGTTCAACAATGGGCTAAGAGCGCAAGG	1260
QY	2153	ATGATCTTGATTAAGAGAAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTAATGGCTGCT	2212
Db	1261	ATGATCTTGATTAAGAGAAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTAATGGCTGCT	1320

OY 2213 TGTGGCGTTTCGCACTAAGAAAGTACATTGCTTTTATCGCCCACTGGAA CGCAGACCT 2272
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Db 1321 TGTGGCGTTTCGCACTAAGAAAGTACATTGCTTTATCGCCCACTGGAA CGCAGACCT 1380
OY 2273 GCGTAAAGTCCAGACCTCTTTTAGCGCTTTTCCATGTCGTCCTATGACGACCTCTT 2332
|||
Db 1381 GCGTAAAGTCCAGACCTCTTTTAGCGCTTTTCCATGTCGTCCTATGACGACCTCTT 1440
OY 2333 TGCCCATGTCGTGAGCGAGAAATTGAAATGCACTTGCAACCAAGAAAGAGAAAAAC 2392
|||
Db 1441 TGCCCATGTCGTGAGCGAGAAATTGAAATGCACTTGCAACCAAGAAAGAGAAAAAC 1500
OY 2393 TGCTGACAGTCTCGAGAGGAATTAGTCATGAGGCCAAGGCTGCTTTTGAGATGCTCAGG 2452
|||
Db 1501 TGCTGACAGTCTCGAGAGGAATTAGTCATGAGGCCAAGGCTGCTTTTGAGATGCTCAGG 1560
OY 2453 AGGAAGCCAGAGCGGAGAGAACTCCGAGAAAGCACTTCCACATTAGTGAGACAAAGGCA 2512
|||
Db 1561 AGGAAGCCAGAGCGGAGAGAACTCCGAGAAAGCACTTCCACATTAGTGAGACAAAGGCA 1620
OY 2513 TCGAGGCAAGCCGAGAAAGTTGTCTGCGAAAGTGAGGGGCTCCAGGCGGACATCGAGCAG 2572
|||
Db 1621 TCGAGGCAAGCCGAGAAAGTTGTCTGCGAAAGTGAGGGGCTCCAGGCGGACATCGAGCAG 1680
OY 2573 CATTAGTTGAACCCCGCGCGGTACAGTAAGATTAATACCTCAAGCAATGACCGTATGA 2632
|||
Db 1681 CATTAGTTGAACCCCGCGCGGTACAGTAAGATTAATACCTCAAGCAATGACCGTATGA 1740
OY 2633 TCGGACAGTATATCGTTGTCTCGCCAACTGTGTCTGAAGAATGCCAACTCGCACAG 2692
|||
Db 1741 TCGGACAGTATATCGTTGTCTCGCCAACTGTGTCTGAAGAATGCCAACTCGCACAG 1800
OY 2693 CGCACCCGCTAGACGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGGTACG 2752
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Db 1801 CGCACCCGCTAGACGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGGTACG 1860
OY 2753 CGGTGGAACCATACGACGCTAAAGTACTGATGCGACGAGAGGTGCGTACATGCGCAG 2812
|||
Db 1861 CGGTGGAACCATACGACGCTAAAGTACTGATGCGACGAGAGGTGCGTACATGCGCAG 1920
OY 2813 AATTCTAGCACTGAGTGAGAGCGCCACGTTAGTGTAACAAGAAAGAGGTTTGTAACC 2872
|||
Db 1921 AATTCTAGCACTGAGTGAGAGCGCCACGTTAGTGTAACAAGAAAGAGGTTTGTAACC 1980
OY 2873 GCAAACTATACCACTATGCGCATGATGCGCCCGCCCAAGAATACAGAAGAGCAAGTACA 2932
|||
Db 1981 GCAAACTATACCACTATGCGCATGATGCGCCCGCCCAAGAATACAGAAGAGCAAGTACA 2040
OY 2933 AGGTACAAGGAGAGAGCTTGCAAAAAGAGTACGTTTGACGTGACAGAAGAGCGTT 2992
|||
Db 2041 AGGTACAAGGAGAGAGCTTGCAAAAAGAGTACGTTTGACGTGACAGAAGAGCGTT 2100
OY 2993 GCGTTAAGAGAGAAAGCCTCAGTCTGCTCTCGGAGAACTGACCAACCTCCCT 3052
|||
Db 2101 GCGTTAAGAGAGAAAGCCTCAGTCTGCTCTCGGAGAACTGACCAACCTCCCT 2160
OY 3053 ATCATGAGCTAGCTCTGAGAGGAGCTGAAGACCGACCTGCGGTCCCTACAAGGTGAAA 3112
|||
Db 2161 ATCATGAGCTAGCTCTGAGAGGAGCTGAAGACCGACCTGCGGTCCCTACAAGGTGAAA 2220
OY 3113 CAATAGAGTGAAGGACACACCGGGGTGCGGCAAGTCAAGTATTAAGTCAACTGTCA 3172
|||
Db 2221 CAATAGAGTGAAGGACACACCGGGGTGCGGCAAGTCAAGTATTAAGTCAACTGTCA 2280
OY 3173 CGGCACGAGATCTTGTATCCAGCGGAAAGAAATTTGTGCGGAATGAGGCGGAGC 3232
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Db 2281 CGGCACGAGATCTTGTATCCAGCGGAAAGAAATTTGTGCGGAATGAGGCGGAGC 2340
OY 3233 TGCTAAGACTGAGGGGTATGAGATTACGTGGAAGACAGTAGATTGCTTAACG 3292
|||
Db 2341 TGCTAAGACTGAGGGGTATGAGATTACGTGGAAGACAGTAGATTGCTTAACG 2400

OY 3293 GATGCCACAAGCCGTAGAAAGTGTCTGATCTTGACGAAGCGTTGCGGTGCCAGCAGAG 3352
|||
Db 2401 GATGCCACAAGCCGTAGAAAGTGTCTGATCTTGACGAAGCGTTGCGGTGCCAGCAGAG 2460
OY 3353 CACTACTTGCTTGATTGCTATCGTACAGGCCCGCAAGAAGTAGTACTATGCGGAGACC 3412
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Db 2461 CACTACTTGCTTGATTGCTATCGTACAGGCCCGCAAGAAGTAGTACTATGCGGAGACC 2520
OY 3413 CCATGCAATGCGGATTTCTTCAACATGATGCAACTAAAGTACATTTCAATCAACCTGAAA 3472
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Db 2521 CCATGCAATGCGGATTTCTTCAACATGATGCAACTAAAGTACATTTCAATCAACCTGAAA 2580
OY 3473 AAGACATATGACCAAGACATTTCTACAATATCTCCGCGCTTGACACAGCCAGTTA 3532
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Db 2581 AAGACATATGACCAAGACATTTCTACAATATCTCCGCGCTTGACACAGCCAGTTA 2640
OY 3533 CAGCTATTGTATCGACACTGCAATTAAGTGAAGAAATGAAAAACCAAGAACCCGTGCAAGA 3592
|||
Db 2641 CAGCTATTGTATCGACACTGCAATTAAGTGAAGAAATGAAAAACCAAGAACCCGTGCAAGA 2700
OY 3593 AGAATTTGAATCGATATTTACAGGGGCCCAAAAGCCGAAGCCAGGGATATCATCTCTGA 3652
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Db 2701 AGAATTTGAATCGATATTTACAGGGGCCCAAAAGCCGAAGCCAGGGATATCATCTCTGA 2760
OY 3653 CATGTTCCGCGGGTGGTTAAGCAATTTGCAATCGACTATCCCGACATGAAGTAAATGA 3712
|||
Db 2761 CATGTTCCGCGGGTGGTTAAGCAATTTGCAATCGACTATCCCGACATGAAGTAAATGA 2820
OY 3713 CAGCCGCGCTCACAAGGGCTAAACCAAGAAAGAGTGTATGCGGTCCGCAAAAAAGTCA 3772
|||
Db 2821 CAGCCGCGCTCACAAGGGCTAAACCAAGAAAGAGTGTATGCGGTCCGCAAAAAAGTCA 2880
OY 3773 ATGAAAACCCACTGTACGCGATCAATGATGCAATGTAAGCGTTGCTCAACCCGCACTG 3832
|||
Db 2881 ATGAAAACCCACTGTACGCGATCAATGATGCAATGTAAGCGTTGCTCAACCCGCACTG 2940
OY 3833 AGGACAGGCTAGTGTGAAAAACCTTGCAAGGCGACCCATGATTAAGCCCACTAACA 3892
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OY 3893 TACCTAAAGAACTTTACAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATTA 3952
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Db 3001 TACCTAAAGAACTTTACAGGCTACTATAGAGGACTGGGAAGCTGAACACAAGGGAATTA 3060
OY 3953 TTGCTGCAATTAACAGCCCACTCCCGCTGCAATCCGTTACGCTGCAAGCAACGCTT 4012
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Db 3061 TTGCTGCAATTAACAGCCCACTCCCGCTGCAATCCGTTACGCTGCAAGCAACGCTT 3120
OY 4013 GCTGGCGAAAGATTTGGAACCGATACCTAGCCAGCGCGGTATCGTACTTACCGGTTGCC 4072
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Db 3121 GCTGGCGAAAGATTTGGAACCGATACCTAGCCAGCGCGGTATCGTACTTACCGGTTGCC 3180
OY 4073 AGTGAGCGAAGTGTCCCAAGTTTCCGATGACAAACCAATTCGCGCATTTACGCCCT 4132
|||
Db 3181 AGTGAGCGAAGTGTCCCAAGTTTCCGATGACAAACCAATTCGCGCATTTACGCCCT 3240
OY 4133 TAGACGTAATTGCAATTAAGTTTTCGGCATGACTTGACAAGCGGACTGTTTCTAAAC 4192
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Db 3241 TAGACGTAATTGCAATTAAGTTTTCGGCATGACTTGACAAGCGGACTGTTTCTAAAC 3300
OY 4193 AGAGCATCCCACTAACGTACCATCCCGCGCATTCAGCGAGCGCGTACATTTGGGACA 4252
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Db 3301 AGAGCATCCCACTAACGTACCATCCCGCGCATTCAGCGAGCGCGTACATTTGGGACA 3360
OY 4253 ACAGCCAGGAACCCGCAAGTATGGTACGATCAAGCCATTCGCGCGCACTCTCCGTA 4312
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Db 3361 ACAGCCAGGAACCCGCAAGTATGGTACGATCAAGCCATTCGCGCGCACTCTCCGTA 3420
OY 4313 GATTTCCGCTTCCAGCTAGCTGGGAAGGACACAACTTGATTTGCAACGGGAGAA 4372
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Db 3421 GATTTCCGCTTCCAGCTAGCTGGGAAGGACACAACTTGATTTGCAACGGGAGAA 3480
OY 4373 CCAGAGTTATCTTGACACAGCATTAACCTGCTCCCGGTGAACCGCAATCTTCTCAGCCCT 4432

Db 3481 CCAGAGTTATCTCTGCACAGCATTAACCTGTGCCGGTGAACCGCAATCTTCTCACGCCCT 3540
QY 4433 TAGTCCCGGAGTACAAGAGAACACCCGGCCGGTCAAAAATTTCTTGAACCACTTCA 4492
Db 3541 TAGTCCCGGAGTACAAGAGAACACCCGGCCGGTCAAAAATTTCTTGAACCACTTCA 3600
QY 4493 AACACCACTCAGTACTTGTGTATCAGAGAAAAAATTGAAGTCCCCGTAAGAGATCG 4552
Db 3601 AACACCACTCAGTACTTGTGTATCAGAGAAAAAATTGAAGTCCCCGTAAGAGATCG 3660
QY 4553 AATGATCGCCCCGATTTGGCATAGCCGGTGCAGATAAGAACTAACCTGGCTTTGGGT 4612
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QY 4613 TTCCGCGGACGGCAGGTACGACCTGGTGTTCATCAACATTGGAATAATACAGAAACC 4672
Db 3721 TTCCGCGGACGGCAGGTACGACCTGGTGTTCATCAACATTGGAATAATACAGAAACC 3780
QY 4673 AACCACTTCAGCAGTGCAGAACCAATGCGGCGACCTTAAAAACCTTTCGCGTTCGCC 4732
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QY 4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTCCGACAACTAGACAAACAGCC 4912
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Db 4021 GTACACGGCAATTCAACCCGACCATCTGAATTGCGTATTCGCTGATGAGGTA 4080
QY 4973 CAAGAGATGAGTTGGAGCCGCGCGTCATACCGCACCAAAAGGAGAAATATTGCTGACT 5032
Db 4081 CAAGAGATGAGTTGGAGCCGCGCGTCATACCGCACCAAAAGGAGAAATATTGCTGACT 4140
QY 5033 GTCAAGAGAGACAGTTGTCAACGACGCCAATCCGCTGGGTAGACCAAGCGAAGACTCT 5092
Db 4141 GTCAAGAGAGACAGTTGTCAACGACGCCAATCCGCTGGGTAGACCAAGCGAAGACTCT 4200
QY 5093 GCCGTGCATCTATTAACGTTGGCCGACAGTTTACCAGTTCAAGCAACGAGACAGGCA 5152
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QY 5153 CCGCAAGATGACTGTGTGCTAGGAAAGAAAGTGATCCACGCGGTGCGCCCTGATTTC 5212
Db 4261 CCGCAAGATGACTGTGTGCTAGGAAAGAAAGTGATCCACGCGGTGCGCCCTGATTTC 4320
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QY 5333 ACGCAGCCGGAAGAACCGCCTTGAAGTATCACTTAAGTCTTGACAAACCGCGCTAGACA 5392
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Db 4621 ATGAGTTAGTATGATTCATCCAGACAGTGTCTTGAAGGAGAAAGGATTCAGTACTA 4680
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Db 4921 TCCACAGACTTAGAAGCAATTAACGTCAAAAGAGTTACAGTATGCTCTCCACCCCTTC 4980
QY 5873 CTAAAGCACAAAATTGAAGTGTCAAGAGGTTCAAGAGTTCAGTGCAGAAAGTAGTCTGTTAATC 5932
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QY 5933 CGCACACTCCCGCATTCGTTCCCGCCGTAAGTACATAGAGTGCCAGAACGCTTACCG 5992
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QY 5993 CTCTCTCTGCACAGGCGGAGAGGCCCCGGAAGTTGTAGCGACACCGTCAACCATCTACAG 6052
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QY 6053 CTGATTAACACCTCGCTTGATGTCAACAGATCTCACTGATATGATGACAGTACGAAG 6112
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Db 5221 GCTCACTTTTTCGAGCTTTAGCGGATCGGACCACTCTATTACTAGTATGACAAGTTGCT 5280
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Db 5341 ATGCCGTCCAAGAGCCTGCCCTATTCCACCGCAAGGCTAAAGAAAGTGGCCGCGCTGG 5400
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QY 6473 CCGACGAGAGATTGATGAGTGAAGCGCAGAGTAACTGAGTCCGAACCCGCTGTTT 6532
Db 5581 CCGACGAGAGATTGATGAGTGAAGCGCAGAGTAACTGAGTCCGAACCCGCTGTTT 5640
QY 6533 GATCATTTGAACCGGGCGAAGTGAATCAATTATATCGTCCCGATCAGCCGATCTTTTC 6592
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QY 6593 CACTACGCAAGCAGAGACGTAGACGCGAGGAGCAGAGGACTGAATACTGACTAACCGGGG 6652
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QY 6653 TAGGTGGGTACATATTTTCGACGAGACACAGGCCCTGGGCACTTGCAAAAAGAGTCCGTTT 6712
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Db 5761 TAGGTGGGTACATATTTTCGACGAGACACAGGCCCTGGGCACTTGCAAAAAGAGTCCGTTT 5820

QY 6713 TGCAGAACCAAGCTTACAGAACCGACCTTGAGCGGCAATGTCTGGAAGAATTATGCCC 6772
| | | | |
Db 5821 TGCAGAACCAAGCTTACAGAACCGACCTTGAGCGGCAATGTCTGGAAGAATTATGCCC 5880

QY 6773 CGGTGCTGCACACGCTCGAAAGAGAAACAACCTCAACTCAGGTACCAAGATGATGCCACCG 6832
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Db 5881 CGGTGCTGCACACGCTCGAAAGAGAAACAACCTCAACTCAGGTACCAAGATGATGCCACCG 5940

QY 6833 AAGCCAAACAAAGTAGTAGTCCAGTCTCGTAAAGTAGAAATCAGAAAGCCATTAACCACTG 6892
| | | | |
Db 5941 AAGCCAAACAAAGTAGTAGTCCAGTCTCGTAAAGTAGAAATCAGAAAGCCATTAACCACTG 6000

QY 6893 AGCGACTACTGTACGAGCTACGACTGTATTAAGTCTGCCACAGATCAGCCAGATGCTATA 6952
| | | | |
Db 6001 AGCGACTACTGTACGAGCTACGACTGTATTAAGTCTGCCACAGATCAGCCAGATGCTATA 6060

QY 6953 AGATCACCTATCCGAAACCATTTGACTCCAGTAGCGTACCGGCGAACTACTCCGATCCAC 7012
| | | | |
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| | | | |
Db 6121 AGTTGCTGTAGCTGTCTGTAAACAATCTTGCAATGAGAACTATCCGACAGTAGCATCTT 6180

QY 7073 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGTTAGACGAGACAGTCCGATGCC 7132
| | | | |
Db 6181 ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGTTAGACGAGACAGTCCGATGCC 6240

QY 7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTGAAGTTACCCGAAAAACATGAGTATA 7192
| | | | |
Db 6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTGAAGTTACCCGAAAAACATGAGTATA 6300

QY 7193 GAGCCCCGAATATCCGACAGTGGGTTCCATCAAGCATGCAAGACACGCTAACAAATGTGC 7252
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Db 6301 GAGCCCCGAATATCCGACAGTGGGTTCCATCAAGCATGCAAGACACGCTAACAAATGTGC 6360

QY 7253 TCATTGCCGCACTTAAAGAAATTTGCAACGTCACGAGATGCGTGAATGCCAACACTGG 7312
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Db 6361 TCATTGCCGCACTTAAAGAAATTTGCAACGTCACGAGATGCGTGAATGCCAACACTGG 6420

QY 7313 ACTCAGCGACATTCATGTGCAATGCTTTCGAAAATATGCATGTAAATGACGAGTATGGG 7372
| | | | |
Db 6421 ACTCAGCGACATTCATGTGCAATGCTTTCGAAAATATGCATGTAAATGACGAGTATGGG 6480

QY 7373 AGGAGTTCGCTCGAAGCCAAATTAGATTACCACTGAGTTTGTACCGCATATGTAAGCTA 7432
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Db 6481 AGGAGTTCGCTCGAAGCCAAATTAGATTACCACTGAGTTTGTACCGCATATGTAAGCTA 6540

QY 7433 GACTGAAAGGCCCTTAAGCGCGCGCAGCTATTTGCAAAAGACGTATATTTGGTCCCATTTGC 7492
| | | | |
Db 6541 GACTGAAAGGCCCTTAAGCGCGCGCAGCTATTTGCAAAAGACGTATATTTGGTCCCATTTGC 6600

QY 7493 AAGAAGTGCCTATGAGTAGATTGTCATGACATGAAAAAGAGACGTGAAAGTTACACCAAG 7552
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Db 6601 AAGAAGTGCCTATGAGTAGATTGTCATGACATGAAAAAGAGACGTGAAAGTTACACCAAG 6660

QY 7553 GCACGAAACACACAGAAAGAAAGACCGAAAGTACAGTGATACAAAGCCGCAAAACCCCTGG 7612
| | | | |
Db 6661 GCACGAAACACACAGAAAGAAAGACCGAAAGTACAGTGATACAAAGCCGCAAAACCCCTGG 6720

QY 7613 CGACTGCTTACTTATGCGGGATTCAACCGGGAATTAGTGCCTAGGCTTACGCGCGTCTTGC 7672
| | | | |
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| | | | |
Db 6781 TTCCAACATTCACACGCTTTTGTGACATGTCCGCGGAGGATTTTGTATGCAATCATAGCAG 6840

QY 7733 AACACTTCAAGCAAGGCGACCCGGTACTGTGAGACGGATATCGCATCATTCGACAAAAGCC 7792
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RESULT 14
AR282856
LOCUS AR282856 13905 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from patent US 6524792.
ACCESSION AR282856
VERSION AR282856.1 GI:29719658
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13905)
AUTHORS Renner,W.A., Orberger,G.H., Koller,D. and Bailey,J.E.

TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property
JOURNAL Patent: US 6524792-A 1 25-FEB-2003;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 89.4%; Score 7637.4; DB 6; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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LOCUS AR221249 Sequence 102 from patent US 6426196.
DEFINITION AR221249
ACCESSION AR221249
VERSION AR221249.1 GI:23328145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8000)
AUTHORS Dubensky,T.W. Jr., Polo,J.M., Schlesinger,S. and Frolov,I.
TITLE Alphavirus structural protein expression cassettes
JOURNAL Patent: US 6426196-A 102 30-JUL-2002;
FEATURES
source location/Qualifiers
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/organism="unknown"
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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 7639; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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OY 953 TGGAGAAGCCAGTAGTAACGTAGACGTAGACCCCCAGAGTCCGTTTGTGCAACTGC 1012
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OY 1013 AAAAAAGCTTCCCGCAATTGAGGTAGTAGCACAAGCAGAGTCACTCCAAATGACCATGCTA 1072
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OY 1313 TCCGACCGTACTTGATACGCCCGGATGTGAACACCATCGCTTGCTTTCACAACGATG 1372
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Db 5461 CTTTGGTGGGTAATCCATGTCCCTCGGATCAATTTTTCGACGAGAGACGGCCCGCAGG 5520
QY 6413 CAGCGGTACAAACCCCTGGCAACAGGCCCCCAGCGGATGTGCTTATGTCTTTGGATCGTTT 6472
Db 5521 CAGCGGTACAAACCCCTGGCAACAGGCCCCCAGCGGATGTGCTTATGTCTTTGGATCGTTT 5580
QY 6473 CCGACGAGAGATGTAGCTGAGCCGCGAGAGTAAGTCCGAAACCGTCTGTTTG 6532
Db 5581 CCGACGAGAGATGTAGCTGAGCCGCGAGAGTAAGTCCGAAACCGTCTGTTTG 5640
QY 6533 GATCATTTGAACCGGCGGAAGTGAACCTCAATTATATCGTCCCGATCAGCCGTATCTTTTC 6592
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QY 7013 AGTTGCTGTAGCTGTCTGTAAACAATATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
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Db 6541 GACTGAAAGGCCCTAAGCCCGCCGCACTATTGCAAAAGCCTATATTTGTCCTCATTTGC 6600
QY 7493 AAGAGTGCTATGATGATGATTTGTCATGAGCATGAAAGAGACGTGAAGTTACACCAAG 7552
Db 6601 AAGAGTGCTATGATGATGATTTGTCATGAGCATGAAAGAGACGTGAAGTTACACCAAG 6660
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Db 6661 GCACGAAACACACAGAGAAAGACCGAAAGTATCAAGAGTATCAAGCCGAGAACCCCTGG 6720
QY 7613 CGACTGCTTACTTATGCGGGAATTCACCGGGAATTAAGTGAAGCTTACCGCCGCTTTC 7672
Db 6721 CGACTGCTTACTTATGCGGGAATTCACCGGGAATTAAGTGAAGCTTACCGCCGCTTTC 6780
QY 7673 TTCCAACATTCACACGCTTTTTCATGATGTCGGCGGAGAGTTTGTGCAATCATAGCAG 7732
Db 6781 TTCCAACATTCACACGCTTTTTCATGATGTCGGCGGAGAGTTTGTGCAATCATAGCAG 6840
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QY 7793 AAGACGACGCTATGCGCTTAAACCGGCTGATGATCTTTGAGAGACCTGGGTGTGATCAAC 7852
Db 6901 AAGACGACGCTATGCGCTTAAACCGGCTGATGATCTTTGAGAGACCTGGGTGTGATCAAC 6960
QY 7853 CACTACTGACTTGAATGAGTGCCTTTGAGAAATATCATCCACCATCTACCTACCG 7912
Db 6961 CACTACTGACTTGAATGAGTGCCTTTGAGAAATATCATCCACCATCTACCTACCG 7020
QY 7913 GTACTGTTTTTAATTCGGGCGATGATGAATCCGAAATGTTCTCACAATTTTGTCA 7972
Db 7021 GTACTGTTTTTAATTCGGGCGATGATGAATCCGAAATGTTCTCACAATTTTGTCA 7080

QY 7973 ACACAGTTTGAATGTCGTTATCGCCAGAGAGTACTAGAAAGAGCGGCTTAAAACGTCCA 8032
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 Db 7261 GTGAGAGACCACTTACTTCTGCGGCGGATTTATCTTGCAAGATTGGGTTACTTCCACAG 7320
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 Db 7561 TCAGAGGGGAAATAAAGCATCTCTACGGTGTCTTAATAGTCAGCATAGTACATTTTCAT 7620
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 QY 8513 CTGACTAATACTACAACACCAACCACC 8538
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 Db 7621 CTGACTAATACTACAACACCAACCACC 7646
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 Job time : 23457 secB

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 16275 Seconds
(without alignments)
19971.170 Million cell updates/sec

Title: US-09-275-883-1_COPY_1_8539

Perfect score: 8539
Sequence: 1 ctgacgcgcctctgtagcgc.....atactacacaccacacct 8539

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	gb_est2:*
3:	gb_hic:*
4:	gb_est3:*
5:	gb_est4:*
6:	gb_est5:*
7:	gb_est6:*
8:	gb_gse1:*
9:	gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
C 1	616.8	7.2	813	7 CN385673	CN385673 LE2TR04D2
C 2	616.8	7.2	860	7 CV089193	CV089193 est_c_vir
C 3	616.8	7.2	862	7 CN385663	CN385663 LE2TR04D1
C 4	616.8	7.2	874	7 CN385637	CN385637 LE2TR04C0
C 5	616.8	7.2	884	7 CN385877	CN385877 LE2TR04M1
C 6	616.8	7.2	899	7 CN385574	CN385574 LE2TR03P1
C 7	616.8	7.2	921	7 CN384456	CN384456 LE2TR01A0
C 8	608.8	7.1	805	2 BE421195	BE421195 HMM006.G0
C 9	607.8	7.1	685	5 BU724260	BU724260 SJMBFC05
C 10	607.8	7.1	702	6 CB549906	CB549906 MMPL0007
C 11	607.8	7.1	714	6 CB548528	CB548528 MMPL0022
C 12	607.8	7.1	753	5 BQ157858	BQ157858 NF103A09P
C 13	607.8	7.1	758	5 BQ158943	BQ158943 NF095D07P
C 14	607.8	7.1	764	5 BQ158750	BQ158750 NF070F07P
C 15	607.8	7.1	771	5 BQ158875	BQ158875 NF076G06P
C 16	607.8	7.1	773	5 BQ156760	BQ156760 NF096H04I
C 17	607.8	7.1	774	5 BQ158974	BQ158974 NF098A06P
C 18	607.8	7.1	775	5 BQ158844	BQ158844 NF073D03P
C 19	607.8	7.1	776	5 BQ159296	BQ159296 NF092H12P
C 20	607.8	7.1	779	5 BQ158936	BQ158936 NF083H10P
C 21	607.8	7.1	782	5 BQ158981	BQ158981 NF099E10P
C 22	607.8	7.1	794	5 BQ158923	BQ158923 NF083A12P
C 23	607.8	7.1	795	5 BQ157846	BQ157846 NF098C12P
C 24	607.8	7.1	799	1 AV405326	AV405326 AV405326

C 25	607.8	7.1	810	7 CV478551	CV478551 Lu6B6 FlA
C 26	607.8	7.1	815	7 CV478075	CV478075 Lu1A6 FlA
C 27	606.8	7.1	757	5 BQ158987	BQ158987 NF100G10P
C 28	606.8	7.1	758	5 BQ159010	BQ159010 NF102E04P
C 29	606.8	7.1	762	5 BQ158850	BQ158850 NF073H10P
C 30	606.8	7.1	768	5 BQ158329	BQ158329 NF047G06P
C 31	606.8	7.1	769	5 BQ159407	BQ159407 NF120B04P
C 32	606.8	7.1	770	5 BQ158852	BQ158852 NF074B11P
C 33	606.8	7.1	771	5 BQ158940	BQ158940 NF095A10P
C 34	606.8	7.1	776	5 BQ158753	BQ158753 NF071A06P
C 35	606.8	7.1	777	5 BQ159021	BQ159021 NF103G05P
C 36	606.8	7.1	779	5 BQ159399	BQ159399 NF118A11P
C 37	606.8	7.1	781	5 BQ158877	BQ158877 NF076G10P
C 38	606.8	7.1	781	5 BQ159263	BQ159263 NF090H06P
C 39	606.8	7.1	782	5 BQ158858	BQ158858 NF075C06P
C 40	606.8	7.1	784	5 BQ158848	BQ158848 NF074A07P
C 41	606.8	7.1	784	5 BQ158973	BQ158973 NF098A03P
C 42	606.8	7.1	786	5 BQ159035	BQ159035 NF104H08P
C 43	606.8	7.1	788	5 BQ158195	BQ158195 NF031B09P
C 44	606.8	7.1	792	5 BQ158756	BQ158756 NF071E09P
C 45	606.8	7.1	799	5 BQ158971	BQ158971 NF097D10P

ALIGNMENTS

RESULT 1
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LOCUS CN385673 813 bp mRNA linear EST 31-AUG-2004
DEFINITION LE2TR04D22 Tomato CL5915 roots under different developmental stages
ACCESSION CN385673
VERSION CN385673
KEYWORDS CN385673.1 GI:51700987
SOURCE EST.
ORGANISM Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 813)
Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
DNA microarray profiling of gene expression during tomato root
development
Unpublished (2004)
Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of BioAgricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyo@gate.sinica.edu.tw
Insert Length: 813 Std Error: 0.00
Plate: 04 row: D column: 22
Seq primer: smart2.
Location/Qualifiers
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/clone="LE2TR04D22"
/tissue_type="roots"
/dev_stage="1-,2-,3-, and 4- month-old"
/lab_host="E.coli BM25.8"
/clone_lib="Tomato CL5915 roots under different
developmental stages"
/note="Vector: pTribEx2; Tomato CL5915 seeds are obtained
from AVRDC.Roots were harvested from plants grown under
different developmental stages: 1-,2-,3-,4-month-old.
Equal aliquots of mRNA of different developmental stages
were mixed and used for cDNA library construction. (Smart
PCR cDNA Library construction kit, Clontech)"

ORIGIN

Query Match	7.2%;	Score 616.8;	DB 7;	Length 813;
Best Local Similarity	97.4%;	Pred. No. 1.5e-174;		
Matches 627;	Conservative	0;	Mismatches 17;	Indels 0;
				Gaps 0;

QY	3	GACGGCCCTGTAGCGGCGCATTTAAGCGCGCGGGTGTGTGTTACGGCAGCGGTACC	62
Db	699	GACGGCCCTGTAGCGGCGCATTTAAGCGCGCGGGTGTGTGTTACGGCAGCGGTACC	640
QY	63	GCTACACTTGCCAGCGCCCTAGCGCCCGCTCTTTCCGCTTTCTTCCCTTCTTCGCC	122
Db	639	GCTACACTTGCCAGCGCCCTAGCGCCCGCTCTTTCCGCTTTCTTCCCTTCTTCGCC	580
QY	123	ACGTTCCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTAGGGTTCCGATTT	182
Db	579	ACGTTCCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTAGGGTTCCGATTT	520
QY	183	AGTGTCTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGTTACGTAAGTGG	242
Db	519	AGTGTCTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGTTACGTAAGTGG	460
QY	243	CCATCGCCCTGATAGACGGTTTTTTCGCCCTTGAAGTGGAGTCCACGTTCTTTAATAGT	302
Db	459	CCATCGCCCTGATAGACGGTTTTTTCGCCCTTGAAGTGGAGTCCACGTTCTTTAATAGT	400
QY	303	GGACTCTGTCTCCAACTGGAACAACACTCAACCTATCTCGTCTATTCTTTGATTTA	362
Db	399	GGACTCTGTCTCCAACTGGAACAACAACACTCAACCTATCTCGTCTATTCTTTGATTTA	340
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Db	339	TAAAGGATTTTGCCGATTTTCGGCTATTGGTTAAAAATGAGCTGATTTAACAAAAATTT	280
QY	423	AACGCGAATTTTAACAAAATATTAAAGCTTACAAATTTCCATTGCGCATTCAGGCTGCCA	482
Db	279	AACGCGAATTTTAACAAAATATTAAAGCTTACAAATTTCCATTGCGCATTCAGGCTGCCA	220
QY	483	ACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCCAAAGGG	542
Db	219	ACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCCAAAGGG	160
QY	543	GATGTGCTGCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTTCCAGTACGACGTGTGA	602
Db	159	GATGTGCTGCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTTCCAGTACGACGTGTGA	100
QY	603	AAACGACGGCCAGTGAGCGCGCAATTAACCTCACTAAAGGGAA	646
Db	99	AAACGACGGCCAGTGGAATTTGTAATACGACTCACTATAGGGCGAA	56

RESULT 2
CV089193/c
LOCUS
DEFINITION
CV089193 860 bp mRNA linear EST 26-AUG-2004
est_c_virginica2856 Cv Hepatopancreas Crassostrea virginica cDNA,
mRNA sequence.
ACCESSION
CV089193
VERSION
CV089193.1 GI:51568542
KEYWORDS
EST.
SOURCE
Crassostrea virginica (eastern oyster)
ORGANISM
Crassostrea virginica
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
Ostreoidea; Ostreidae; Crassostrea.
REFERENCE
1 (bases 1 to 860)
AUTHORS
Jenny, M.J., Warr, G.W., Gross, P.S., Almeida, J.S., Chen, Y.,
McKillen, D.J., Wu, S. and Chapman, R.W.
TITLE
Crassostrea virginica EST Library at marinegenomics.org
JOURNAL
Unpublished (2004)
COMMENT
Contact: Gross PS
Department of Biochemistry and Molecular Biology
Medical University of South Carolina
Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA
Tel: 846 792 8503
Fax: 843 792 4850

Email: grossp@usc.edu.
Location/Qualifiers
1. .860

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/organism="Crassostrea virginica"
/mol_type="mRNA"
/db_xref="taxon:6565"
/cell_type="hepatopancreas"
/clone_lib="Cv Hepatopancreas"
/note="Vector: pTriplex2; Site_1: Sfi I; Site_2: Sfi I"
ORIGIN

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Query Match	7.2%;	Score 616.8;	DB 7;	Length 860;
Best Local Similarity	97.4%;	pred. No. 1.6e-174;		
Matches 627;	Conservative	0;	Mismatches 17;	Indels 0;
				Gaps 0;

QY	3	GAGCGCCCTGTAGCGCGCATTTAAGCGCGCGGGTGTGTGTGTAAAGCCGACCGTGACC	62
Db	707	GACGCGCCCTGTAGCGCGCATTTAAGCGCGCGGGTGTGTGTGTAAAGCCGACCGTGACC	648
QY	63	GCTACACTTGGCAGCGCCCTAGCGCCCGCTCCTTTGCGTTTCTTCCCTTCTTCTCGCC	122
Db	647	GCTACACTTGGCAGCGCCCTAGCGCCCGCTCCTTTGCGTTTCTTCCCTTCTTCTCGCC	588
QY	123	ACGTTGCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTAGGGTTCGATTT	182
Db	587	ACGTTGCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTAGGGTTCGATTT	528
QY	183	AGTCTTTACGGCACTTCGACCCCAAAAACTTGATTAAGGTGATGTTCACGTAGTGGG	242
Db	527	AGTCTTTACGGCACTTCGACCCCAAAAACTTGATTAAGGTGATGTTCACGTAGTGGG	468
QY	243	CCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT	302
Db	467	CCATCGCCCTGATAGACGGTTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGT	408
QY	303	GGACTCTTGTTCCAAACCTGGAACAACACTCAACCTTACTCGGTCTATTCTTTGATTTA	362
Db	407	GGACTCTTGTTCCAAACCTGGAACAACACTCAACCTTACTCGGTCTATTCTTTGATTTA	348
QY	363	TAAGGATTTTGC CGATTTTCGGCTATTGTTAAAAATGAGCTGATTTTAACAAAAATTT	422
Db	347	TAAGGATTTTGC CGATTTTCGGCTATTGTTAAAAATGAGCTGATTTTAACAAAAATTT	288
QY	423	AACGGAATTTTAACAAATATTTAACGCTTACAATTTCCATTCCGCAATTCAGGCTCGCA	482
Db	287	AACGGAATTTTAACAAATATTTAACGCTTACAATTTCCATTCCGCAATTCAGGCTCGCA	228
QY	483	ACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG	542
Db	227	ACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG	168
QY	543	GATGTGCTGCAAGCGCATTTAAGTTGGGTAAAGCCAGGGTTTTCCCAAGTCAGACGTTGTA	602
Db	167	GATGTGCTGCAAGCGCATTTAAGTTGGGTAAAGCCAGGGTTTTCCCAAGTCAGACGTTGTA	108
QY	603	AAACGACGGCGCAGTGAGCGCGCAATTAACCTCTCTAAAGGGAA	646
Db	107	AAACGACGGCGCAGTGAAATTTGTAATACGACTCACTAATAGGGCGAA	64

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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	CN385563	862 bp	mrna	linear	EST 31-AUG-2004		
	LE2TR04D12	Tomato	CL5915	roots under different developmental stages			
	Lycopersicon	esculentum	cdna	clone LE2TR04D12,	mrna sequence.		
	CN385563						
	CN385563.1	GI:51700977					
	EST.						
	Lycopersicon	esculentum	(tomato)				
	Lycopersicon	esculentum					
	Eukaryota;	Viridiplantae;	Streptophyta;	Embryophyta;	Tracheophyta;		
	Spermatophyta;	Magnoliophyta;	eudicotyledons;	core eudicots;			
	asterids;	lamids;	Solanales;	Solanaceae;	Solanum;	Lycopersicon.	

REFERENCE 1 (bases 1 to 862)
AUTHORS Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of Bioagricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyo@gate.sinica.edu.tw
Insert Length: 862 Std Error: 0.00
Plate: 04 row: D column: 12
Seq primer: smart2.
Location/Qualifiers
FEATURES
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/cultivar="CL5915"
/db_xref="taxon:4081"
/clone="LE2TR04D12"
/tissue_type="roots"
/dev_stage="1-,2-,3-, and 4- month-old"
/lab_host="E.coli BM25.8"
/clone_lib="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained from AVRDC.Roots were harvested from plants grown under different developmental stages: 1-,2-,3-,4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"
ORIGIN
Query Match 7.2%; Score 616.8; DB 7; Length 862;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 3 GACGGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGTGTTACGGCAGCGTGACC 62
DB 699 GACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGTGTTACGGCAGCGTGACC 640
QY 63 GCTACACTTGGCAGCGCCCTAGCGCCGCTTTCGCTTCTTCCCTTCTTCTCGCC 122
DB 639 GCTACACTTGGCAGCGCCCTAGCGCCGCTTTCGCTTCTTCCCTTCTTCTCGCC 580
QY 123 ACGTTGCGCGCTTTCGCCGTCAAGCTCTAAATCGGGGCTCCCTTAAAGGTTCCGATT 182
DB 579 ACGTTGCGCGCTTTCGCCGTCAAGCTCTAAATCGGGGCTCCCTTAAAGGTTCCGATT 520
QY 183 AGTGCCTTACGCGACCTTCGACCCCAAAAACCTGATTAGGGTGATGATTCACGTAGTGG 242
DB 519 AGTGCCTTACGCGACCTTCGACCCCAAAAACCTGATTAGGGTGATGATTCACGTAGTGG 460
QY 243 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTCACGTTGGAGTCCACGTTCTTAAATAGT 302
DB 459 CCATCGCCCTGATAGACGGTTTTTCGCCCTTTCACGTTGGAGTCCACGTTCTTAAATAGT 400
QY 303 GGACTCTTGTTCAAAACCTGGAACACACTCAACCTATCTCGGTCTATTCTTTGATTTA 362
DB 399 GGACTCTTGTTCAAAACCTGGAACACACTCAACCTATCTCGGTCTATTCTTTGATTTA 340
QY 363 TAAGGATTTTGGCGATTTCGGCTATTGTTAAAAATGAGCTGATTAACAAAAATTT 422
DB 339 TAAGGATTTTGGCGATTTCGGCTATTGTTAAAAATGAGCTGATTAACAAAAATTT 280
QY 423 AACGGAATTTTAACAAAATATTAAAGCTTACATTTCCATTGCGCATTCAGGCTGCGCA 482
DB 279 AACGGAATTTTAACAAAATATTAAAGCTTACATTTCCATTGCGCATTCAGGCTGCGCA 220
QY 483 ACTGTTGGAAGGGGATCGGTGCGGCTCTTCGTATTACGCCAGCTGGCGAAGGGG 542
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DB 219 ACTGTTGGAAGGGGATCGGTGCGGCTCTTCGTATTACGCCAGCTGGCGAAGGG 160
QY 543 GATGTGCTGCAAGCGCATTAAGTTGGGTAAACGCCAGGTTTCCACGTACGACGTGTA 602
DB 159 GATGTGCTGCAAGCGCATTAAGTTGGGTAAACGCCAGGTTTCCACGTACGACGTGTA 100
QY 603 AAACGACGGCAGTGAGCGCGCAATTAACCTCACTAAAGGAA 646
DB 99 AAACGACGGCAGTGAAATTGTAATACGACTACTATAGGCGGA 56
RESULT 4
CN385637/c 874 bp mRNA linear EST 31-AUG-2004
LOCUS LE2TR04C09 Tomato CL5915 roots under different developmental stages
DEFINITION Lycopersicon esculentum cDNA clone LE2TR04C09, mRNA sequence.
ACCESSION CN385637
VERSION CN385637.1 GI:51700951
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 874)
AUTHORS Wang,C.K., Chen,P.Y., Wang,H.M., Soong,S.C., Chen,S.C. and To,K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of Bioagricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyo@gate.sinica.edu.tw
Insert Length: 874 Std Error: 0.00
Plate: 04 row: C column: 09
Seq primer: smart2.
Location/Qualifiers
FEATURES
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/organism="Lycopersicon esculentum"
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/cultivar="CL5915"
/db_xref="taxon:4081"
/clone="LE2TR04C09"
/tissue_type="roots"
/dev_stage="1-,2-,3-, and 4- month-old"
/lab_host="E.coli BM25.8"
/clone_lib="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained from AVRDC.Roots were harvested from plants grown under different developmental stages: 1-,2-,3-,4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)"
ORIGIN
Query Match 7.2%; Score 616.8; DB 7; Length 874;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 3 GACGGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGTGTTACGGCAGCGTGACC 62
DB 699 GACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGTGTTACGGCAGCGTGACC 640
QY 63 GCTACACTTGGCAGCGCCCTAGCGCCGCTTTCGCTTCTTCCCTTCTTCTCGCC 122
DB 639 GCTACACTTGGCAGCGCCCTAGCGCCGCTTTCGCTTCTTCCCTTCTTCTCGCC 580
QY 123 ACGTTGCGCGCTTTCGCCGTCAAGCTCTAAATCGGGGCTCCCTTAAAGGTTCCGATT 182
|||||

Db 579 ACGTCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTCCGATT 520

QY 183 AGTGCTTTACGGCACTCTCGACCCCAAAAAGTTGATTAGGGTGATGGTTCAAGTAGTGG 242

Db 519 AGTGCTTTACGGCACTCTCGACCCCAAAAAGTTGATTAGGGTGATGGTTCAAGTAGTGG 460

QY 243 CCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCCAGCTTCTTAATAGT 302

Db 459 CCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCCAGCTTCTTAATAGT 400

QY 303 GGACTCTTGTCCAAACTGGAACAACACTCAACCTATCTCGCTATCTTTGATT 362

Db 399 GGACTCTTGTCCAAACTGGAACAACACTCAACCTATCTCGCTATCTTTGATT 340

QY 363 TAAGGATTTTGGCCGATTTCGCCCTATTGTTAAAAATGAGCTGATTAAACAAAATTT 422

Db 339 TAAGGATTTTGGCCGATTTCGCCCTATTGTTAAAAATGAGCTGATTAAACAAAATTT 280

QY 423 AACGGAATTTTAAACAAATATTAAACGCTTACATTTCCATTCCGCAATTCAGGCTGCGCA 482

Db 279 AACGGAATTTTAAACAAATATTAAACGCTTACATTTCCATTCCGCAATTCAGGCTGCGCA 220

QY 483 ACTGTTGGGAAGGCGCATCGTGCGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGG 542

Db 219 ACTGTTGGGAAGGCGCATCGTGCGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGG 160

QY 543 GATGTGCTGCAAGCGCATTAAGTTGGTTAACGCCAGGGTTTCCAGTCAGCAGCTTGTA 602

Db 159 GATGTGCTGCAAGCGCATTAAGTTGGTTAACGCCAGGGTTTCCAGTCAGCAGCTTGTA 100

QY 603 AAACGACGGCCAGTGAGCGCGCAATTAAACCTCACTAAAGGGA 646

Db 99 AAACGACGGCCAGTGAAATTGTAATACGACTCATATAGGCGGA 56

RESULT 5
CN385877/c 884 bp mRNA linear EST 31-AUG-2004
LOCUS LE2TR04M16 Tomato CL5915 roots under different developmental stages
DEFINITION Lycopersicon esculentum cDNA clone LE2TR04M16, mRNA sequence.
CN385877
ACCESSION CN385877.1 GI:51701191
VERSION EST.
KEYWORDS Lycopersicon esculentum (tomato)
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 884)
AUTHORS Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of Bioagricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyo@gate.sinica.edu.tw
Insert Length: 884 Std Error: 0.00
Plate: 04 row: M column: 16
Seq primer: smart2.
location/Qualifiers
1. 884
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
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/db_xref="taxon:4081"
/clone="LE2TR04M16"
/tissue_type="roots"
/dev_stage="1-, 2-, 3-, and 4- month-old"
/lab_host="E.coli BM25.8"

/clone_lib="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplex2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-, 2-, 3-, 4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA library construction kit, Clontech)"

ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 884;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 3 GACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGTTACGCCGACGTAAC 62

Db 699 GACGCGCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGTTACGCCGACGTAAC 640

QY 63 GCTACACTTGGCAGCGCCCTAGCGCCCGCTCTTTCGCTTCTTCCCTTCTCGCC 122

Db 639 GCTACACTTGGCAGCGCCCTAGCGCCCGCTCTTTCGCTTCTTCCCTTCTCGCC 580

QY 123 ACGTTGCGCGCTTTCGCCCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTCCGATT 182

Db 579 ACGTTGCGCGCTTTCGCCCTCAAGCTCTAAATCGGGGCTCCCTTTAGGGTCCGATT 520

QY 183 AGTGCTTTACGGCACCTCGACCCCAAAAAGTTGATTAGGGTGATGTTACAGTAGTGG 242

Db 519 AGTGCTTTACGGCACCTCGACCCCAAAAAGTTGATTAGGGTGATGTTACAGTAGTGG 460

QY 243 CCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGAGTCCAGCTTCTTAATAGT 302

Db 459 CCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGAGTCCAGCTTCTTAATAGT 400

QY 303 GGAATCTTGTCCAACTGGAACAACACTCAACCTATCTCGCTATTCTTTGATT 362

Db 399 GGAATCTTGTCCAACTGGAACAACACTCAACCTATCTCGCTATTCTTTGATT 340

QY 363 TAAGGATTTTGGCCGATTTCGCCCTATTGTTAAAAATGAGCTGATTAAACAAAATTT 422

Db 339 TAAGGATTTTGGCCGATTTCGCCCTATTGTTAAAAATGAGCTGATTAAACAAAATTT 280

QY 423 AACGGAATTTTAAACAAATATTAAACGCTTACATTTCCATTCCGCAATTCAGGCTGCGCA 482

Db 279 AACGGAATTTTAAACAAATATTAAACGCTTACATTTCCATTCCGCAATTCAGGCTGCGCA 220

QY 483 ACTGTTGGGAAGGCGCATCGTGCGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGG 542

Db 219 ACTGTTGGGAAGGCGCATCGTGCGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGG 160

QY 543 GATGTGCTGCAAGCGCATTAAGTTGGTTAACGCCAGGGTTTCCAGTCAGCAGCTTGTA 602

Db 159 GATGTGCTGCAAGCGCATTAAGTTGGTTAACGCCAGGGTTTCCAGTCAGCAGCTTGTA 100

QY 603 AAACGACGGCCAGTGAGCGCGCAATTAAACCTCACTAAAGGGA 646

Db 99 AAACGACGGCCAGTGAAATTGTAATACGACTCATATAGGCGGA 56

RESULT 6
CN385574 899 bp mRNA linear EST 31-AUG-2004
LOCUS LE2TR03P18 Tomato CL5915 roots under different developmental stages
DEFINITION Lycopersicon esculentum cDNA clone LE2TR03P18, mRNA sequence.
CN385574
ACCESSION CN385574.1 GI:51700888
VERSION EST.
KEYWORDS Lycopersicon esculentum (tomato)
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 899)

AUTHORS Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of Bioagricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyo@gate.sinica.edu.tw
Insert Length: 899 Std Error: 0.00
Plate: 03 row: P column: 18
Seq primer: smart2.

FEATURES
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/organism="Lycopersicon esculentum"
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/db_xref="taxon:4081"
/clone="LE2TR03P18"
/tissue_type="roots"
/dev_stage="1-, 2-, 3-, and 4 - month-old"
/lab_host="E.coli BM25.8"
/clone_lib="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-, 2-, 3-, 4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA library construction kit, Clontech)"

ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 899;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 3 GACGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGTGTGTAGCGCGCAGCGTGACC 62
DB 699 GACGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGTGTGTAGCGCGCAGCGTGACC 640
OY 63 GCTACACTTGCCAGCGCCCTAGCGCCGCTCTTTCGCTTCTCCCTTCTTCTCGCC 122
DB 639 GCTACACTTGCCAGCGCCCTAGCGCCGCTCTTTCGCTTCTCCCTTCTTCTCGCC 580
OY 123 ACGTTCGCGGCTTTCCTCCGTCAGCTCTAAATCGGGGGCTCCCTTTAGGGTCCGATT 182
DB 579 ACGTTCGCGGCTTTCCTCCGTCAGCTCTAAATCGGGGGCTCCCTTTAGGGTCCGATT 520
OY 183 AGTGCCTTACGGCACCCTCGACCCCAAAAATTGATTAGGGTGATGTTCAAGTAGGG 242
DB 519 AGTGCCTTACGGCACCCTCGACCCCAAAAATTGATTAGGGTGATGTTCAAGTAGGG 460
OY 243 CCATCGCCCTGATAGACGGTTTTCGCTTTCGAGTTCAGCTTCCTTAAATAGT 302
DB 459 CCATCGCCCTGATAGACGGTTTTCGCTTTCGAGTTCAGCTTCCTTAAATAGT 400
OY 303 GGAATCTGTTCCTCAAACTGGACCAACACCTATCTCGTCTAATCTTTGATTTA 362
DB 399 GGAATCTGTTCCTCAAACTGGACCAACACCTATCTCGTCTAATCTTTGATTTA 340
OY 363 TAAGGATTTGCGGATTTTCGGCTATTTGTTAAAAATGAGCTGATTTAACAAAATTT 422
DB 339 TAAGGATTTGCGGATTTTCGGCTATTTGTTAAAAATGAGCTGATTTAACAAAATTT 280
OY 423 AACGCGAATTTAACAAAATATTAAAGCTTACCAATTTCCATTGCGCATTCAGGCTGCGCA 482
DB 279 AACGCGAATTTAACAAAATATTAAAGCTTACCAATTTCCATTGCGCATTCAGGCTGCGCA 220
OY 483 ACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
DB 219 ACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGGG 160

OY 543 GATGCTGCAAGCGGATTAAGTTGGGTAAAGCCAGGGTTTCCAGTCACGACGTTGTA 602
DB 159 GATGCTGCAAGCGGATTAAGTTGGGTAAAGCCAGGGTTTCCAGTCACGACGTTGTA 100
OY 603 AAACGAGCGCCAGTGAGCGCGCAATTAAACCTTCACTAAAGGGA 646
DB 99 AAACGAGCGCCAGTGAGTTGTAATACGACTCATATAGGCGCA 56

RESULT 7
CN384456/c 921 bp mRNA linear EST 31-AUG-2004
LOCUS
DEFINITION LE2TR01A01 Tomato CL5915 roots under different developmental stages
ACCESSION Lycopersicon esculentum cDNA clone LE2TR01A01, mRNA sequence.
VERSION CN384456
KEYWORDS CN384456.1 GI:51699770
SOURCE EST.
ORGANISM Lycopersicon esculentum (tomato)
Lycopersicon esculentum

REFERENCE
AUTHORS Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of Bioagricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2561-5600
Email: kyo@gate.sinica.edu.tw
Insert Length: 921 Std Error: 0.00
Plate: 01 row: A column: 01
Seq primer: smart2.

FEATURES
Source

1. 921
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="CL5915"
/db_xref="taxon:4081"
/clone="LE2TR01A01"
/tissue_type="roots"
/dev_stage="1-, 2-, 3-, and 4 - month-old"
/lab_host="E.coli BM25.8"
/clone_lib="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-, 2-, 3-, 4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA library construction kit, Clontech)"

ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 921;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 3 GACGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGTGTGTAGCGCGCAGCGTGACC 62
DB 699 GACGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGTGTGTAGCGCGCAGCGTGACC 640
OY 63 GCTACACTTGCCAGCGCCCTAGCGCCGCTCTTTCGCTTCTTCCCTTCTTCTCGCC 122
DB 639 GCTACACTTGCCAGCGCCCTAGCGCCGCTCTTTCGCTTCTTCCCTTCTTCTCGCC 580
OY 123 ACGTTCGCGGCTTTCCTCCGTCAGGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGATT 182
DB 579 ACGTTCGCGGCTTTCCTCCGTCAGGCTCTAAATCGGGGGCTCCCTTTAGGGTTCGATT 520


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QY 183 AGTCTTTACGGGACCTCGACCCCAAAAACTTGATTAGGGTGATGTTCAAGTAGTGGG 242
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Db 519 AGTCTTTACGGGACCTCGACCCCAAAAACTTGATTAGGGTGATGTTCAAGTAGTGGG 460
QY 243 CCATCGCCCTGTAGACGGTTTTTGGCCCTTTGACGTTGAGTCCAGCTTCTTTAATAGT 302
    |||
Db 459 CCATCGCCCTGTAGACGGTTTTTGGCCCTTTGACGTTGAGTCCAGCTTCTTTAATAGT 400
QY 303 GGACTCTTGTCCAAACTGGAACAACACTCAACCCCTATCTCGGTCTATCTTTGATTTA 362
    |||
Db 399 GGACTCTTGTCCAAACTGGAACAACACTCAACCCCTATCTCGGTCTATCTTTGATTTA 340
QY 363 TAAGGATTTTGGCCGATTTTCGGCCTATTGGTTAAAAATGAGCTGATTTAACAAAAATT 422
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Db 339 TAAGGATTTTGGCCGATTTTCGGCCTATTGGTTAAAAATGAGCTGATTTAACAAAAATT 280
QY 423 AACGCGAATTTTAACAAAATATTAAACGCTTACATTTCCATTCCGCAATTCAGGCTGCGA 482
    |||
Db 279 AACGCGAATTTTAACAAAATATTAAACGCTTACATTTCCATTCCGCAATTCAGGCTGCGA 220
QY 483 ACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGG 542
    |||
Db 219 ACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAGGG 160
QY 543 GATGTCGTGAAGGCGATTAAAGTTGGGTAACGCCAGGTTTTCCAGTCACGAGCTTGT 602
    |||
Db 159 GATGTCGTGAAGGCGATTAAAGTTGGGTAACGCCAGGTTTTCCAGTCACGAGCTTGT 100
QY 603 AAACGAGCGCCAGTGAGCGCGCAATTAAACCTCACTAAAGGGA 646
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Db 99 AAACGAGCGCCAGTGAGATTGTAATACGACTCACTATAGGGCGAA 56
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RESULT 8
BE421195/c 805 bp mRNA linear EST 24-JUL-2000
LOCUS HMM006.G08 ITEC HMM Barley Leaf Library Hordeum vulgare subsp.
DEFINITION vulgare cDNA clone HMM006.G08, mRNA sequence.
ACCESSION BE421195
VERSION BE421195.1 GI:9419038
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Hordeum.
REFERENCE
1 (bases 1 to 805)
Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,
Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,
Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,
Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P.,
Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,
Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
International Triticaceae EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticaceae
Unpublished (2000)
JOURNAL Contact: Herrmann RG
COMMENT Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
Fax: 49 30 171683
Email: herrmann@botanik.biologie.uni-muenchen.de
International Triticaceae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
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FEATURES
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/organism="Hordeum vulgare subsp. vulgare"
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/db_xref="taxon:112509"
/clone="HMM006.G08"
/tissue_type="leaf"
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/note="Vector: pBluescriptSK(-); 850 bp average insert
size."
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ORIGIN
Query Match 7.1%; Score 608.8; DB 2; Length 805;
Best Local Similarity 99.4%; Pred. No. 4.1e-172;
Matches 621; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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QY 1 CTGACGCGCCCTGTAGCGGCATTAAGCGCGCGGTGTGTGTTACGCGCAGCGTGA 60
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Db 777 CTGACGCGCCCTGTAGCGGCATTAAGCNCGCCGGGTGTGTGTTACGCGCAGCGTGA 718
QY 61 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCTTTCGCTTCTTCCCTTCTCTCG 120
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Db 717 CCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCTTTCGCTTCTTCCCTTCTCTCG 658
QY 121 CCACGTTGCCCGGCTTTCCTCCCTCAAGCTCTAAATCGGGGGCTCCCTTAGGGTTCCGAT 180
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Db 657 CCACGTTGCCCGGCTTTCCTCCCTCAAGCTCTAAATCGGGGGCTCCCTTAGGGTTCCGAT 598
QY 181 TTAGTCTTTACGGGACCTCGACCCCAAAAACTTGATTAGGGTGATGTTACGTAAGTG 240
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Db 597 TTAGTCTTTACGGGACCTCGACCCCAAAAACTTGATTAGGGTGATGTTACGTAAGTG 538
QY 241 GGCCATCGCCCTGTAGACGGTTTTTTCGCCCTTTCGAGTTCAGTCCAGTCTTTAATA 300
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Db 537 GGCCATCGCCCTGTAGACGGTTTTTTCGCCCTTTCGAGTTCAGTCCAGTCTTTAATA 478
QY 301 GTGACTCTTGTTCCAAACCTGGAACAACACTCAACCTATCTCGTCTATTCTTTGATT 360
    |||
Db 477 GTGACTCTTGTTCCAAACCTGGAACAACACTCAACCTATCTCGTCTATTCTTTGATT 418
QY 361 TATAAGGATTTTGGCCGATTTTCGGCCTATTGGTT-AAAAATGAGCTGATTTAACAAAA 419
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Db 417 TATAAGGATTTTGGCCGATTTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAA 358
QY 420 TTTAACGCGAATTTTAACAAATATTTAACGCTTACATTTCCATTGCGCCATTGAGGCTGC 479
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Db 357 TTTAACGCGAATTTTAACAAATATTTAACGCTTACATTTCCATTGCGCCATTGAGGCTGC 298
QY 480 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAG 539
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Db 297 GCAACTGTTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGAAAG 238
QY 540 GGGGATGTGTCGCAAGCGGATTAAAGTTGGGTAACGCCAGGGTTTTCCAGTCAGACGTT 599
    |||
Db 237 GGGGATGTGTCGCAAGCGGATTAAAGTTGGGTAACGCCAGGGTTTTCCAGTCAGACGTT 178
QY 600 GTAAAAAGACGGCCAGTGAGCGCGC 624
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Db 177 GTAAAAAGACGGCCAGTGAGCGCGC 153
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RESULT 9
BU724260/c 685 bp mRNA linear EST 23-OCT-2003
LOCUS SJBFC05 SUM Schistosoma japonicum cDNA similar to gb|AAB53629.1|
DEFINITION (U84006) beta-galactosidase [Expression vector pBSII-LUCINT], mRNA
sequence.
ACCESSION BU724260
VERSION BU724260.1 GI:28331629
KEYWORDS EST.
SOURCE Schistosoma japonicum
ORGANISM Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
REFERENCE
1 (bases 1 to 685)
Hu,W., Yan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R.,
Wang,Z.J., Rong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J.,
Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J.,
McManus,D.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.
```

TITLE Evolutionary and biomedical implications of a Schistosoma japonicum
Complementary DNA resource
JOURNAL Nat. Genet. 35 (2), 139-147 (2003)
MEDLINE 22879925
PUBMED 12973349
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.

FEATURES
Source Location/Qualifiers
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/organism="Schistosoma japonicum"
/mol_type="mRNA"
/db_xref="taxon:6182"
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ORIGIN

Query Match 7.1%; Score 607.8; DB 5; Length 685;
Best Local Similarity 97.2%; Pred. No. 7.8e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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DB 615 CCGCTACACTTGCCAGCGCCCTAGCGCCGCTCTTTCGCTTCTCCCTCTTCTCG 556
OY 121 CCACGTTGCGCGGCTTTCCCGCTCAAGCTTAATCGGGGCTCCCTTTAGGGTCCGAT 180
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DB 555 CCACGTTGCGCGGCTTTCCCGCTCAAGCTTAATCGGGGCTCCCTTTAGGGTCCGAT 496
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OY 241 GGCCATCGCCCTGATAGACGTTTTCGCCCTTGACGTTGAGTCCAGTCTTTAATA 300
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DB 435 GGCCATCGCCCTGATAGACGTTTTCGCCCTTGACGTTGAGTCCAGTCTTTAATA 376
OY 301 GTGACTCTTGTTCCAACTGGAACAACACTCAACCTATCTCGGTCTATTCTTTGATT 360
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DB 375 GTGACTCTTGTTCCAACTGGAACAACACTCAACCTATCTCGGTCTATTCTTTGATT 316
OY 361 TATAAGGATTTTGCCGATTTGCGGCTATTGTTAAAAATGAGCTGATTAAACAAAAT 420
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DB 315 TATAAGGATTTTGCCGATTTGCGGCTATTGTTAAAAATGAGCTGATTAAACAAAAT 256
OY 421 TTAACGCGAATTTTAACAAATATTAAACGCTTACAATTT-CCATTGCGCATTCAGGCTGC 479
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DB 255 TTAACGCGAATTTTAACAAATATTAAACGCTTACAATTTGCCATTGCGCATTCAGGCTGC 196
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DB 195 GCAACTGTTGGGAAGGGCGATCGTGGCGGCTCTTCGCTATTACGCCAGCTGGCGAAG 136
OY 540 GGGGATGTGCTGCAAGCGGATTAAGTTGGGTTAACGCCAGGGTTTCCAGTCAAGAGCTT 599
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DB 135 GGGGATGTGCTGCAAGCGGATTAAGTTGGGTTAACGCCAGGGTTTCCAGTCAAGAGCTT 76
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RESULT 10

CB549906 702 bp mRNA linear EST 01-JUN-2003
LOCUS MMPL0007_B01 MPPL Macaca mulatta cDNA, mRNA sequence.
DEFINITION CB549906
ACCESSION CB549906
VERSION CB549906.1 GI:31299101
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.

1 (bases 1 to 702)

REFERENCE Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and

AUTHORS Holzman, T.

Expressed sequence tags from Rhesus macaque placenta
Unpublished (2003)

COMMENT Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055

Email: ted@locke.hs.washington.edu
Similar to GenBank entry HSU94592 U94592 Human uncoupling protein
homolog (UCPH) mRNA, complete cds. 6/2002
Plate: MMPL0007 row: B Column: 01.

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Source Location/Qualifiers
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/sex="male"
/dev_stage="neonatal"
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/note="Organ: Placenta"

ORIGIN

Query Match 7.1%; Score 607.8; DB 6; Length 702;
Best Local Similarity 97.2%; Pred. No. 7.9e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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DB 669 CTGACGCGCCCTGTAGCGCGCATTAAGCGCGGGGTGTGTGTTACGCGACGCTGA 610
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DB 549 CCACGTTGCGCGGCTTTCCCGCTCAAGCTTAATCGGGGCTCCCTTTAGGGTCCGAT 490
OY 181 TTAGTGCTTTACGGCACCTCGACCCCAAAAATTGATTAGGTGATGTTACGTAAGT 240
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DB 489 TTAGTGCTTTACGGCACCTCGACCCCAAAAATTGATTAGGTGATGTTACGTAAGT 430
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DB 309 TATAAGGATTTTGCCGATTTGCGGCTATTGTTAAAAATGAGCTGATTAAACAAAAT 250
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QY 480 GCAACTGTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTACGCCAGCTGGCGGAAG 539
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QY 540 GGGGATGTGCTGCAAGCGGATTAAGTTGGGTAAACGCCAGGGTTTCCCACTACGACGTT 599
| | | | |
Db 129 GGGGATGTGCTGCAAGCGGATTAAGTTGGGTAAACGCCAGGGTTTCCCACTACGACGTT 70
QY 600 GTAAACGACGCGCAGTGAAGCGCAATTAACCTCACTAAAGGGA 646
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Db 69 GTAAACGACGCGCAGTGAATTTGTAATACGACTCATATAGGCGGA 23
RESULT 11
CB548528/c 714 bp mRNA linear EST 01-JUN-2003
LOCUS MMPL0022_H09 MMPL Macaca mulatta cDNA, mRNA sequence.
DEFINITION CB548528
ACCESSION CB548528
VERSION CB548528.1 GI:31297723
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 714)
AUTHORS Katze,M.G., Bumgarner,R., Korth,M., Feldman,R., Amjadi,M. and
Holzman,T.
TITLE Expressed sequence tags from Rhesus macaque placenta
JOURNAL Unpublished (2003)
COMMENT Contact: Holzman T
Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hs.washington.edu
Similar to GenBank entry HSU94592 U94592 Human uncoupling protein
homolog (UCPH) mRNA, complete cds. 6/2002
FEATURES
source 1. 714
location/Qualifiers
/organism="Macaca mulatta"
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/note="Organ: placenta"
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Query Match 7.1%; Score 607.8; DB 6; Length 714;
Best Local Similarity 97.2%; Pred. No. 7.9e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
QY 1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGGGGGGTGTGTGTTAGCGGACGCTGA 60
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QY 121 CCACGTTGCGCGGCTTTCGCCGCTCAAGCTCTAATCGGGGCTCCCTTAGGGTTCCGAT 180
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Db 582 CCACGTTGCGCGGCTTTCGCCGCTCAAGCTCTAATCGGGGCTCCCTTAGGGTTCCGAT 523
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Db 402 GTGACTCTTGTGTTCCAACTGGAACAACACTCAACCTATCTCGGTCTATTCTTTGATT 343
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Db 342 TATAAGGATTTTGCCGATTTTCGGCTATTGTTAAAAAATGAGCTGATTAACAAAAAT 283
QY 421 TTAACGGGAATTTTAACAATAATTAACGCTTACAATTT-CCATTGCCATTCAAGCTGC 479
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Db 282 TTAACGGGAATTTTAACAATAATTAACGCTTACAATTTGCCATTGCCATTCAAGCTGC 223
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| | | | |
Db 162 GGGGATGTGCTGCAAGCGGATTAAGTTGGGTAAACGCCAGGGTTTCCCACTACGACGTT 103
QY 600 GTAAACGACGCGCAGTGAAGCGCAATTAACCTCACTAAAGGGA 646
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Db 102 GTAAACGACGCGCAGTGAATTTGTAATACGACTCATATAGGCGGA 56
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BQ157858/c 753 bp mRNA linear EST 24-APR-2002
LOCUS NF103A09PL1067 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION BQ157858
ACCESSION BQ157858
VERSION BQ157858.1 GI:20294915
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 753)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Imman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula phosphate-starved leaf library
COMMENT Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 753 Std Error: 0.00
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/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

ORIGIN

Query Match 7.1%; Score 607.8; DB 5; Length 753;
Best Local Similarity 97.2%; Pred. No. 8.1e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGGCGGGGTGTGGTTACGCGCAGCGTGA 60
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QY 61 CCGCTACACTTGCCAGCGCCCTAGCGCCGCTCTTCCCTTCTTCCCTTCTCTCG 120
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QY 121 CCACGTCGCGCGCTTCCCGCTCAAGCTCTAATCGGGGCTCCCTTAGGGTCCGAT 180
DB 628 CCACGTCGCGCGCTTCCCGCTCAAGCTCTAATCGGGGCTCCCTTAGGGTCCGAT 569
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QY 241 GGCCATCGCCCTGATAGACGGTTTTCGCCCTTGACGCTTGAGTCCACGTTCTTAATA 300
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QY 301 GTGACTCTGTGCCAACTGGAACAACCTAATCTGCTCTATCTTTGATT 360
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QY 361 TATAAGGATTTTGGCGATTTGGCTATTGTTAAAAATGAGCTGATTTAACAAAAAT 420
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QY 421 TTAACGCGAATTTTAACAATAATTAACGCTTACAATTT-CCATTGCCATTGAGGCTGC 479
DB 328 TTAACGCGAATTTTAACAATAATTAACGCTTACAATTTGCCATTGCCATTGAGGCTGC 269
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DB 268 GCAACTGTGGGAAGGGCGATCGGTGGGGCTCTTCCGCTATTACGCCAGCTGGCGAAG 209
QY 540 GGGATGTGCTGCAAGGCGCATTAAGTGGGTAAAGCCAGGGTTTCCAGTACGAGCTT 599
DB 208 GGGATGTGCTGCAAGGCGCATTAAGTGGGTAAAGCCAGGGTTTCCAGTACGAGCTT 149
QY 600 GTAAACGACGGCCAGTAGAGCGCGCAATTAAACCTCACTAAAGGAA 646
DB 148 GTAAACGACGGCCAGTAGAGTTGTAATACGACTACTATAGGGCGAA 102

RESULT 13
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LOCUS NF095D07PL1F1060 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION clone NF095D07PL 5', mRNA sequence.

ACCESSION BQ158943
VERSION BQ158943.1 GI:20296000
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 758)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula phosphate-starved leaf library
COMMENT Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
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Seq primer: TCACACAGGAACAGCTATGAC.
Location/Qualifiers

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source

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/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

ORIGIN

Query Match 7.1%; Score 607.8; DB 5; Length 758;
Best Local Similarity 97.2%; Pred. No. 8.1e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 CTGACGCGCCCTGTAGCGGCGCATTAAGCGGCGGGGTGTGGTTACGCGCAGCGTGA 60
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QY 61 CCGCTACACTTGCCAGCGCCCTAGCGCCGCTCTTCCCTTCTTCCCTTCTCTCG 120
DB 687 CCGCTACACTTGCCAGCGCCCTAGCGCCGCTCTTCCCTTCTTCCCTTCTCTCG 628
QY 121 CCACGTCGCGCGCTTCCCGCTCAAGCTCTAATCGGGGCTCCCTTAGGGTCCGAT 180
DB 627 CCACGTCGCGCGCTTCCCGCTCAAGCTCTAATCGGGGCTCCCTTAGGGTCCGAT 568
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DB 327 TTAACGCGAATTTTAACAATAATTAACGCTTACAATTTGCCATTGCCATTGAGGCTGC 268
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DB 267 GCAACTGTGGGAAGGGCGATCGGTGGGGCTCTTCCGCTATTACGCCAGCTGGCGAAG 208
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DB 147 GTAAACGACGGCCAGTAGAGTTGTAATACGACTACTATAGGGCGAA 101

RESULT 14
LOCUS BQ158750/c
DEFINITION BQ158750 764 bp mRNA linear EST 24-APR-2002
clone NF070F07PL1061 Phosphate starved leaf Medicago truncatula cDNA
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VERSION BQ158750.1 GI:20295807
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 764)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula phosphate-starved leaf library
COMMENT Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 764 Std Error: 0.00
Plate: 070 row: F column: 07
Seq primer: TCACACAGGAACACGCTATGAC.
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/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

ORIGIN
Query Match 7.1%; Score 607.8; DB 5; Length 764;
Best Local Similarity 97.2%; Pred. No. 8.1e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
QY 1 CTGACGGCCCTGTAGCGCGCATTAAGCGCGGTGTGTGTTACGCGCAGCGTGA 60
Db |||||
748 CTGACGGCCCTGTAGCGCGCATTAAGCGCGGTGTGTGTTACGCGCAGCGTGA 689
QY 61 CCGCTACACTTGCCAGCGCCCTAGCGCCGCTCTTCCCTTCTCCCTTCTCTCG 120
Db |||||
688 CCGCTACACTTGCCAGCGCCCTAGCGCCGCTCTTCCCTTCTCTCCCTTCTCTCG 629
QY 121 CCAGTTGCGCGGCTTCCCGTCAAGCTCTAATCGGGGCTCCCTTAGGGTTCCGAT 180
Db |||||
628 CCAGTTGCGCGGCTTCCCGTCAAGCTCTAATCGGGGCTCCCTTAGGGTTCCGAT 569
QY 181 TTAGTGCTTTACGGCACCCTGACCCCAAAAACCTGATTAGGGTGATGTTACGTA 240
Db |||||
568 TTAGTGCTTTACGGCACCCTGACCCCAAAAACCTGATTAGGGTGATGTTACGTA 509
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Db |||||
448 GTGACTCTTGTTCACAACTGGAACAACACTCAACCTATCTCGTCTATTCTTTGATT 389
QY 361 TATAAGGATTTTGCCTGATTTCCGCTATTGGTTAAAAATGAGCTGATTACAAAAT 420
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388 TATAAGGATTTTGCCTGATTTCCGCTATTGGTTAAAAATGAGCTGATTACAAAAT 329
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328 TTAACGCGAATTTTACAAATATTAAACGCTTACAAATTGCCATTGGCCATTGAGCTGC 269
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Db |||||
268 GCAACTGTTGGGAAGGCGCATCGGTGCGGCTCTTCTGCTATTACGCCAGCTGCGAAAG 209
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Db |||||
208 GGGATGTGCTGCAAGCGGATTAAGTTGGTTAACGCCAGGTTTCCAGTCACGACGTT 149
QY 600 GTAAACGACGGCCAGTGAGCGCGCAATTAAACCTCACTAAAGGAA 646
Db |||||
148 GTAAACGACGGCCAGTGATTTGTAATACGACTCACTATAGGGCGAA 102

RESULT 15
LOCUS BQ158875/c
DEFINITION BQ158875 771 bp mRNA linear EST 24-APR-2002
clone NF076G06PL1050 Phosphate starved leaf Medicago truncatula cDNA
BQ158875
VERSION BQ158875
KEYWORDS BQ158875.1 GI:20295932
SOURCE EST.
ORGANISM Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 771)
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula phosphate-starved leaf library
COMMENT Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 771 Std Error: 0.00
Plate: 076 row: G column: 06
Seq primer: TCACACAGGAACACGCTATGAC.
FEATURES
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/db_xref="taxon:3880"
/clone="NF076G06PL"
/tissue_type="leaf"
/dev_stage="trifoliolate"
/clone_lib="Phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

ORIGIN
Query Match 7.1%; Score 607.8; DB 5; Length 771;
Best Local Similarity 97.2%; Pred. No. 8.2e-172;

	Matches	629;	Conservative	0;	Mismatches	17;	Indels	1;	Gaps	1;
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Db	690	CCGCTACACTTGCCAGCGCGCCCTAGCGCGCGCTCTTCCGCTTCTCCCTTCTCTCG								631
QY	121	CCACGTTGCGCGGCTTTCGCCGTCAGCTCTAAATCGGGGCTCCCTTTAGGGTCCGAT								180
Db	630	CCACGTTGCGCGGCTTTCGCCGTCAGCTCTAAATCGGGGCTCCCTTTAGGGTCCGAT								571
QY	181	TTAGTGTCTTACGGACCTCGACCCCAAAAATTGATTAGGTGATGTTACAGTAGTG								240
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Db	390	TATAAGGATTTTGCCGATTTCCGCTATTGTTAAAAATGAGCTGATTTAACAAAAAT								331
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Db	210	GGGATGTGCTGCAAGGCGATTAAGTTGGTTAACGCCAGGGTTTCCAGTCAAGACGTT								151
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Search completed: March 23, 2005, 17:05:35
 Job time : 16279 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 2688 Seconds
(without alignments)
18805.309 Million cell updates/sec

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Perfect score: 8539
Sequence: 1 ctgacgcgcctctgtacgagc.....atactacaaccaccacct 8539

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13:	geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8539	100.0	11282	2	AAZ27850 Complete
2	8539	100.0	11282	4	AAD04741 Alphavira
3	8539	100.0	11282	5	AAF84024 Complete
4	8539	100.0	11282	12	ADL71889 Temperatu
5	7657.2	89.7	13068	12	ADL71890 Temperatu
6	7657.2	89.7	15081	12	ADL71909 Expressio
7	7657.2	89.7	17753	12	ADL71910 Expressio
8	7637.4	89.4	9951	2	AAK77354 Polynucle
9	7637.4	89.4	9951	3	AAA90386 Polynucle
10	7637.4	89.4	9951	4	AAD04742 Alphavira
11	7637.4	89.4	9951	6	ABN86686 Nucleotid
12	7637.4	89.4	9951	6	ABV73174 Nucleotid
13	7637.4	89.4	12110	6	ABN86689 Nucleotid
14	7637.4	89.4	13905	2	AAK77358 Polynucle
15	7637.4	89.4	13905	3	AAA90390 Plasmid p
16	7635.8	89.4	10524	2	AAK77355 Polynucle
17	7635.8	89.4	10524	3	AAA90387 Plasmid p
18	7634.8	89.4	8000	8	ABX81525 Sindbis v
19	7634.8	89.4	8000	9	ADA50625 SINGC vir
20	7634.8	89.4	11703	13	ADR32077 Genomic D

21	7634.8	89.4	11703	13	ADR67767	ADR67767 Sindbis v
22	7634.8	89.4	11740	8	ABX81526	ABX81526 Sindbis v
23	7634.8	89.4	11740	9	ADA50626	ADA50626 Toto 1101
24	7634.2	89.4	16847	12	ADO07464	ADO07464 Japanese
25	7632.6	89.4	11927	2	AAK77356	AAK77356 Polynucle
26	7632.6	89.4	11927	3	AAA90388	AAA90388 Plasmid p
27	7623.6	89.3	11703	3	AAC64506	AAC64506 Alphaviru
28	7620.4	89.2	11703	3	AAC64507	AAC64507 Alphaviru
29	7618.8	89.2	11703	2	AAV33476	AAV33476 Sindbis v
30	7617.2	89.2	8000	2	AAK59321	AAK59321 Sindbis v
31	7617.2	89.2	8000	2	AAK58571	AAK58571 Sindbis v
32	7617.2	89.2	8000	8	ABX81524	ABX81524 Sindbis v
33	7617.2	89.2	8000	9	ADA50624	ADA50624 SIN-1 vir
34	7612.4	89.1	16656	2	AAQ86154	AAQ86154 Eukaryoti
35	7612.4	89.1	16656	2	AAV42364	AAV42364 Represent
36	7612.4	89.1	16656	2	AAV60125	AAV60125 Represent
37	7612.4	89.1	16656	2	AAV70684	AAV70684 Represent
38	7612.4	89.1	16656	3	AAZ92892	AAZ92892 Represent
39	7612.4	89.1	16656	3	AAZ92765	AAZ92765 Represent
40	7612.4	89.1	16656	6	AAI38772	AAI38772 DNA of eu
41	7612.4	89.1	16656	12	ADI30344	ADI30344 Eukaryoti
42	7610.8	89.1	16656	6	ABK46238	ABK46238 Eukaryoti
43	7602.8	89.0	16656	2	AAT30787	AAT30787 Alphaviru
44	7598.8	89.0	16958	8	AAI55269	AAI55269 DNA of ex
45	7457	87.3	11687	6	AAD25136	AAD25136 SinChiron

ALIGNMENTS

RESULT 1	AAZ27850	AAZ27850 standard; cDNA; 11282 BP.
ID	AAZ27850;	
AC	AAZ27850;	
XX		
DT	23-DEC-1999	(first entry)
XX		
DE	Complete cDNA sequence of pCYTs.	
XX		
KW	Gene expression system; cis-acting element; gene therapy;	
KW	temperature-sensitive RNA-dependent RNA polymerase;	
KW	inducible alphaviral gene expression system; pCYTs;	
KW	hormone-based gene control system; tetracycline gene control system; ss.	
XX		
OS	Synthetic.	
XX		
XX	WO9950432-A1.	
PN		
PD	07-OCT-1999.	
XX		
PF	25-MAR-1999;	99WO-IB000523.
XX		
PR	27-MAR-1998;	98US-0079562P.
XX		
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.	
PA	(RENN/) RENNER W A.	
PA	(NIEB/) NIEBA L.	
PA	(BOOR/) BOORSMA M.	
XX		
PI	Renner WA, Nieba L, Boorsma M;	
XX		
DR	WPI; 1999-591327/50.	
XX		
PT	A new system to regulate gene expression in eukaryotic cells.	
XX		
PS	Claim 15; Fig 3; 99pp; English.	
XX		
CC	This sequence represents the complete cDNA sequence for the vector	
CC	pCYTs. The invention relates to a DNA molecule comprising a	
CC	polynucleotide (I) encoding an RNA molecule. The encoded RNA comprises:	
CC	(a) at least one cis-acting element; (b) an open reading frame (ORF1)	
CC	encoding a non-cytopathic, temperature-sensitive RNA-dependent RNA	

CC polymerase; and (c) a second sequence that is: (i) a protein-encoding ORF
 CC (ORF2) that is in a translatable format after RNA-dependent RNA
 CC replication event(s); (ii) a sequence complementary to the ORF2; or (iii)
 CC a sequence encoding an untranslated RNA molecule. The pCVTs sequence is
 CC an example of the DNA molecule, and is an inducible alphaviral gene
 CC expression system. The invention is used in gene therapy and recombinant
 CC technology to regulate expression of introduced genes. The invention does
 CC not have the problems of toxicity and/or high basal level expression
 CC associated with prior art tetracycline-based and hormone-based gene
 CC control systems

XX Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 2; Length 11282;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 CCGCTACACTTGCACGCGCCCTAGCGCCCGCTTCTTCCCTTCTTCTCTCTCTCTCTCT 120
 DB 61 CCGCTACACTTGCACGCGCCCTAGCGCCCGCTTCTTCCCTTCTTCTCTCTCTCTCTCT 120
 QY 121 CCACGTTGCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTAGGGTCCGAT 180
 DB 121 CCACGTTGCGCGGCTTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTAGGGTCCGAT 180
 QY 181 TTAGTCTTTACGGGACCTCGACCCCAAAAACTTGATTAGGGTATGTTTACAGTAGTG 240
 DB 181 TTAGTCTTTACGGGACCTCGACCCCAAAAACTTGATTAGGGTATGTTTACAGTAGTG 240
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 DB 241 GGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTAATA 300
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 DB 421 TTAACGCGAATTTTAACAAAATATTTAAGCTTCAATTTCGATTCGCAATTCAGGCTGCG 480
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 DB 481 CAACTGTGGGAAGGGCGATCGGTGCGGGCTCTTCGCTATTAAGCCAGCTGGCGAAAGG 540
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 DB 781 GATCGTGCCTTATTAGGAAGGCAACAGACGGGTCTGACATGGAATTGGACGAACCACTGAA 840

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 QY 1381 AACATGCGTGCCGAATATTCCTGCTATGACAGACGTGATATCAACGCTCCCGGAATATC 1440
 DB 1381 AACATGCGTGCCGAATATTCCTGCTATGACAGACGTGATATCAACGCTCCCGGAATATC 1440
 QY 1441 TATCATCAGGCTATGAAGGGCGTGCGGACCTGTGACTGGATTGGCTTGACACCAACCAG 1500
 DB 1441 TATCATCAGGCTATGAAGGGCGTGCGGACCTGTGACTGGATTGGCTTGACACCAACCAG 1500
 QY 1501 TTGATGTTCTCGGCTATGCGAGGTTCTGTACCTGCGTACCAACCACTGGCGGACGAG 1560
 DB 1501 TTGATGTTCTCGGCTATGCGAGGTTCTGTACCTGCGTACCAACCACTGGCGGACGAG 1560
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Qy 3421 TCGGATTTCTCAACATGATGCAACTAAAGGTACATTTCAATCAACCTGAAAAAGACATA 3480
Db 3421 TCGGATTTCTCAACATGATGCAACTAAAGGTACATTTCAATCAACCTGAAAAAGACATA 3480
Qy 3481 TGCACCAAGACATTTCTACAAGTATATCTCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Db 3481 TGCACCAAGACATTTCTACAAGTATATCTCCGGCGTTGCACACAGCCAGTTACAGCTATT 3540
Qy 3541 GTATCGACACTGCAATTACGATGGAAGATGAAAAACCAAGAACCCGTGCAAGAAACATT 3600
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Db 3721 GCCTCACAAGGCTAACCAAGAAAGAGTGTATGCCGTCCGGCAAAAAAGTCAATGAANAAC 3780
Qy 3781 CCACTGTACCGGATCAATCAGAGCATGTGAACGTGTGCTCACCCGCACTGAGGACAGG 3840
Db 3781 CCACTGTACCGGATCAATCAGAGCATGTGAACGTGTGCTCACCCGCACTGAGGACAGG 3840
Qy 3841 CTAGTGTGAAAACTTGACAGGGCGGACCATGGAATTAAGCAGCCCACTAACATACCTAAA 3900
Db 3841 CTAGTGTGAAAACTTGACAGGGCGGACCATGGAATTAAGCAGCCCACTAACATACCTAAA 3900
Qy 3901 GGAACCTTTCAGGCTACTATAGAGACTGGAAGCTGAACACAAAGGGAATAATTGCTGCA 3960
Db 3901 GGAACCTTTCAGGCTACTATAGAGACTGGAAGCTGAACACAAAGGGAATAATTGCTGCA 3960
Qy 3961 ATAACAGCCCCACTCCCGGTGCCAATCGTTACGCTGCAAGACCAAGCTTGCTGGCGG 4020
Db 3961 ATAACAGCCCCACTCCCGGTGCCAATCGTTACGCTGCAAGACCAAGCTTGCTGGCGG 4020
Qy 4021 AAAGCATTTGAAACCGATACTAGCCACGGCGGATGCTACTTACCGGTTGCCAGTGAGC 4080
Db 4021 AAAGCATTTGAAACCGATACTAGCCACGGCGGATGCTACTTACCGGTTGCCAGTGAGC 4080
Qy 4081 GAACTGTTCCCAAGATTGCGGATGACAAACCAATTGCGGCATTTACGCTTGAACGTA 4140
Db 4081 GAACTGTTCCCAAGATTGCGGATGACAAACCAATTGCGGCATTTACGCTTGAACGTA 4140

QY 4141 ATTTGCATTAAAGTTTTCGGCATGGACTTGACAAGCGGACTGTTTCTAAACAGAGCATC 4200
| | | | |
Db 4141 ATTTGCATTAAAGTTTTCGGCATGGACTTGACAAGCGGACTGTTTCTAAACAGAGCATC 4200
QY 4201 CCACTAACGTACCATCCCGCGATTTCAGCGAGCCGGTAGCTCATTTGGGACAACAGCCCA 4260
| | | | |
Db 4201 CCACTAACGTACCATCCCGCGATTTCAGCGAGCCGGTAGCTCATTTGGGACAACAGCCCA 4260
QY 4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACCTCTCCGTAGATTCCG 4320
| | | | |
Db 4261 GGAACCCGCAAGTATGGGTACGATCACGCCATTGCCGCCGAACCTCTCCGTAGATTCCG 4320
QY 4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACCTTGATTTCAGACGGGGAGAACCAAGATT 4380
| | | | |
Db 4321 GTGTTCCAGCTAGCTGGGAAGGGCACACAACCTTGATTTCAGACGGGGAGAACCAAGATT 4380
QY 4381 ATCTCTGCACAGCATTAACCTGGTCCCGGTGAACCGCAATCTTCTCAGCGCTTAGTCCCC 4440
| | | | |
Db 4381 ATCTCTGCACAGCATTAACCTGGTCCCGGTGAACCGCAATCTTCTCAGCGCTTAGTCCCC 4440
QY 4441 GAGTACAAGAGAGCAACCCCGCCGGTCAAAAAATTTCTTGAACAGTTCAAACACCAC 4500
| | | | |
Db 4441 GAGTACAAGAGAGCAACCCCGCCGGTCAAAAAATTTCTTGAACAGTTCAAACACCAC 4500
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| | | | |
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QY 4561 GCCCCGATTGGCATAGCCCGGTGCAGATAAGAACTACAACCTGGCTTTCCGGTTCCGCCG 4620
| | | | |
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| | | | |
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| | | | |
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| | | | |
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| | | | |
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| | | | |
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Db 5221 CCAGAAACAGAAAGCCTTGAAATTGCTACAAAAACGCTTACCATGCACTGGCAGACTTAGTA 5280
QY 5281 AATGAACATTAACATCAAGTCTGTGCCATTTCACCTGCTATCTACAGGCATTTACGCAACC 5340
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| | | | |
Db 5341 GGAAGAAAGACCGCCTTGAAGTATCACTTAAGTGAAGGAAAGAAATCGACGCGGCACTC 5400
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| | | | |
Db 6181 CCTAGTTCACTAGAGTATGAGACCGGAAGGCAAGTGTGTGCTGACGTTCAATGCCGTC 6240
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| | | | |
Db 6241 CAAGAGCCTGCCCTATTTCCACCGCCAAAGGCTAAAGAAAGTGGCCCGCTGGCAGCGGCA 6300
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Db 6301 AGAAAAAGCCCACTCCACCGCAAGCAATAGCTCTGAGTCCCTCCACTCTCTTTGGT 6360
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Db 6361 GGGGTATCCATGTCCCTCGGATCAATTTTGCAGAGAGACGGCCCGCAGCGGTA 6420
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Db 6421 CAACCCCTGGCAACAGGCCCCACGGATGTGCTTATGTCTTTCGGATCGTTTCCGACGA 6480
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Db 6721 CAGCTTACAGAACCGACCTTGGAGCGCAATGTCTGAAAGAAATTATGCCCCGGTGCTC 6780
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Db 6961 TATCCGAAACCAATTGTACTCCAGTAGCGGCGAACTACTCCGATCCAGTTCGCT 7020
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Db 7021 GTAGCTGTCTGTAACTATCTGATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Qy 7081 ACTGACGAGTACGATGCTTACTTGTGATATGAGAGAGACAGTCCGATGCTGATACT 7140
Db 7081 ACTGACGAGTACGATGCTTACTTGTGATATGAGAGAGACAGTCCGATGCTGATACT 7140
Qy 7141 GCAACCTTCTGCCCCCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATAGAGCCCCG 7200
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Qy 7201 AATATCCGACGTGGGTTCCATCAGCGATGCAACACGCTACAAAATGTCTCATTTGCC 7260
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Qy 7261 GCAACTAAAAAATTGCAAGCTCAGCAGATGCGTGAACCTGCCAACACTGCACTCAGCG 7320
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Qy 7321 ACATTCAATGTGCAATGCTTTGAAAAATATGCAATGATGAGAGTATGGGAGAGGTTT 7380
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Qy 7681 ATTCAACGCTTTTTCACATGTCCGCGAGGATTTTGATGCAATCATAGCAGAACCTTC 7740
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Qy 7741 AAGCAAGCGACCCCGTACTGAGACGATATCGCATCATTCGACAAAGCCAAAGACGAC 7800
Db 7741 AAGCAAGCGACCCCGTACTGAGACGATATCGCATCATTCGACAAAGCCAAAGACGAC 7800
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Db 7801 GCTATGCGCTTAAACCGGTCTGATGATCTTGAAGACCTGGGTGTGATCAACCACTACTC 7860
Qy 7861 GACTTGAATGAGTGGCGCTTTGGAAGAAATATCATCCACCATCTACCGGTACTCGT 7920
Db 7861 GACTTGAATGAGTGGCGCTTTGGAAGAAATATCATCCACCATCTACCGGTACTCGT 7920
Qy 7921 TTTAAATTGCGGGCGATGATGAATCCGGAATGTTCTCTCACACTTTTGTCAACACAGTT 7980
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Qy 7981 TTGAATGCTTATTCGCCAGACAGTACTGAAGAGCGGCTTAAACGTCAGATGTGCA 8040
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Qy 8041 GCGTTCATTGGCGACGACAAACATCATGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Db 8041 GCGTTCATTGGCGACGACAAACATCATGAGTAGTATCTGACAAAGAAATGGCTGAG 8100
Qy 8101 AGGTGCGCACTGCGCTCAACATGAGGTTAAGATCATCGACGCACTCATCGGTGAGAGA 8160
Db 8101 AGGTGCGCACTGCGCTCAACATGAGGTTAAGATCATCGACGCACTCATCGGTGAGAGA 8160
Qy 8161 CCACCTTACTTCTGCGCGGATTTATCTTGAAGATTGCGTTACTTCCACAGCGTGCCGC 8220
Db 8161 CCACCTTACTTCTGCGCGGATTTATCTTGAAGATTGCGTTACTTCCACAGCGTGCCGC 8220
Qy 8221 GTGCGGATCCCTGAAAAAGGCTGTTAAGTTGGGTAAACCGCTCCAGCCGACGAGAG 8280
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Qy 8281 CAAGACGAAAGACAGAAAGCGCTCTGCTAGATGAAACAAAGCGCTGTTAGAGTAGGT 8340
Db 8281 CAAGACGAAAGACAGAAAGCGCTCTGCTAGATGAAACAAAGCGCTGTTAGAGTAGGT 8340
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Qy 8401 GTCTTACTGGCATTGAAACTTTTGCCCAAGACAAAGAGCATTTCCAGCCATCAGAGGG 8460
Db 8401 GTCTTACTGGCATTGAAACTTTTGCCCAAGACAAAGAGCATTTCCAGCCATCAGAGGG 8460
Qy 8461 GAAATTAAGCATCTCTACGGTGTCTTAAATAGTCAGCATAGTACATTTCTGACTAA 8520
Db 8461 GAAATTAAGCATCTCTACGGTGTCTTAAATAGTCAGCATAGTACATTTCTGACTAA 8520

QY 8521 TACTACACACACCACT 8539
Db 8521 TACTACACACACCACT 8539

RESULT 2
AAD04741
ID AAD04741 standard; cDNA; 11282 BP.
XX

AC AAD04741;
XX
DT 17-JUL-2001 (first entry)
XX

DE Alphaviral vector pCYTts cDNA.

KW pCYTts; alphaviral vector; vaccine; therapy; cancer; antiparasitic;
KM antimalarial; anticancer; anti-HIV; antiviral; infectious disease;
KW Human immunodeficiency virus; HIV; influenza; passive immunisation;
KW carcinoma; liver; skin; stomach; ovarian tumour; ss.

OS Rous sarcoma virus.

OS Alphavirus.
OS Unidentified.
OS Chimeric.

PN WO200130989-A2.

PD 03-MAY-2001.

PF 26-OCT-2000; 2000WO-IB001557.

PR 27-OCT-1999; 99US-0161796P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA (RENN/) RENNER W A.
PA (NIEB/) NIEBA L.

PI Renner WA, Nieba L;

DR WPI; 2001-308631/32.

PT Preparing alphaviral vectors with mutations in a selected gene, for use
PT as vaccines, particularly against pathogens that mutate rapidly,
PT comprises replicating in the presence of a nucleoside analog.

PS Claim 6; Fig 3; 103pp; English.

CC The present invention relates to a method for preparing viral vectors
CC which comprises inserting a gene of interest into an alphaviral vector
CC such as pCYTts, pSInRep5 and replicating the vector in the presence of
CC alphaviral replicase and nucleoside analogues (5'azacytidine (AZT), FU-
CC 5' fluorouridine) to produce a modified gene of interest. The replication
CC is repeated until the modified gene in 90 % of the vector population
CC contain a mutation in the modified gene which is 90-99 % identical with
CC the gene of interest. The vector populations are used in vaccines for
CC treatment or prevention of a wide variety of infectious diseases (viral
CC or parasitic, e.g. human immuno deficiency virus (HIV), influenza,
CC Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach
CC carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the
CC mutant populations will therefore be effective against viral escape
CC mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins
CC are correctly glycosylated. Antisera raised against the vaccines can be
CC used for passive immunisation. The present cDNA sequence is an alphaviral
CC vector pCYTts. The vector contains Rous Sarcoma Virus promoter, cis-
CC acting sequence elements, non-structural proteins 1-4, gene of interest,
CC alphavirus subgenomic promoter, ampicillin resistance marker for
CC selection and a ColEI sequence for bacterial amplification

SO Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 4; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;

		Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	CTGACGCGCCCTGTAGCGGCGATTAAAGCGCGGGTGTGTGTACGCGCAGCGTGA	60			
Db	1	CTGACGCGCCCTGTAGCGGCGATTAAAGCGCGGGTGTGTGTACGCGCAGCGTGA	60			
QY	61	CCGCTACCTTGGCAGCGCCCTAGCGCCGCTCTTTCGCTTCTTCTCTCTCG	120			
Db	61	CCGCTACCTTGGCAGCGCCCTAGCGCCGCTCTTTCGCTTCTTCTCTCTCG	120			
QY	121	CGACGTTGCGCGCTTTCGCCGTCAAGCTCTAATCGGGGCTCCCTTAGGGTCCGAT	180			
Db	121	CGACGTTGCGCGCTTTCGCCGTCAAGCTCTAATCGGGGCTCCCTTAGGGTCCGAT	180			
QY	181	TTAGTGCTTTACGGCACTCCGACCCCAAAAACCTTGATTAGGCTGATGTTACGTAAGTG	240			
Db	181	TTAGTGCTTTACGGCACTCCGACCCCAAAAACCTTGATTAGGCTGATGTTACGTAAGTG	240			
QY	241	GGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGAGTCCACGTTCTTTAATA	300			
Db	241	GGCCATCGCCCTGATAGACGGTTTTCGCCCTTTGACGTTGAGTCCACGTTCTTTAATA	300			
QY	301	GTGACTCTTGTTCAAACTGGAACAACACTCAACCTATCTCGGTCTATTCTTTGATT	360			
Db	301	GTGACTCTTGTTCAAACTGGAACAACACTCAACCTATCTCGGTCTATTCTTTGATT	360			
QY	361	TATAAGGATTTTGCCGATTTCCGCCCTATTGTTAAAAATGAGCTGATTTAACAAAAAT	420			
Db	361	TATAAGGATTTTGCCGATTTCCGCCCTATTGTTAAAAATGAGCTGATTTAACAAAAAT	420			
QY	421	TTAAGCGGAATTTTAACAAAATATTAAAGCTTACAATTTCCATTGCGCATTCAGGCTGCG	480			
Db	421	TTAAGCGGAATTTTAACAAAATATTAAAGCTTACAATTTCCATTGCGCATTCAGGCTGCG	480			
QY	481	CAACTGTTGGGAAGGGCGATCGGTGCGGGCTTTCGCTATTACGCCAGCTGCGGAAAG	540			
Db	481	CAACTGTTGGGAAGGGCGATCGGTGCGGGCTTTCGCTATTACGCCAGCTGCGGAAAG	540			
QY	541	GGGATGTGCTGCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTCCAGTCAAGCGTTG	600			
Db	541	GGGATGTGCTGCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTCCAGTCAAGCGTTG	600			
QY	601	TAAACGAGCGCCAGTGAGCGCGCAATTAAACCTCACTAAAGGGAACAAAGCTGGCTAG	660			
Db	601	TAAACGAGCGCCAGTGAGCGCGCAATTAAACCTCACTAAAGGGAACAAAGCTGGCTAG	660			
QY	661	TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGTAAGTTAGCAA	720			
Db	661	TGGATCCAGTCTTATGCAATACTCTTGTAGTCTTGCAACATGTAAGTTAGCAA	720			
QY	721	CATGCCCTTACAAGAGAGAAAAAGCACCGTGATGCCGATTGTTGTAAGTAAGTGTGAC	780			
Db	721	CATGCCCTTACAAGAGAGAAAAAGCACCGTGATGCCGATTGTTGTAAGTAAGTGTGAC	780			
QY	781	GATCGTGCCTTATTAAGGAAGCAACAGACGGGCTGACATGATTTGACGAACCACTGAA	840			
Db	781	GATCGTGCCTTATTAAGGAAGCAACAGACGGGCTGACATGATTTGACGAACCACTGAA	840			
QY	841	TTCCGATTCGAGAGATATTGTATTTAAGTGCCTTACCTCGATACCGGTGAGATTGACGG	900			
Db	841	TTCCGATTCGAGAGATATTGTATTTAAGTGCCTTACCTCGATACCGGTGAGATTGACGG	900			
QY	901	CGTAGTACACACTATTGAATCAAAACAGCGCAATTTGACTACCTACCAATGAGAGAAG	960			
Db	901	CGTAGTACACACTATTGAATCAAAACAGCGCAATTTGACTACCTACCAATGAGAGAAG	960			
QY	961	CCAGTAGTAAACGTAGACGTAGACCCCGAGAGTCCGTTGTGCTGCACTGCAAAAAAGC	1020			
Db	961	CCAGTAGTAAACGTAGACGTAGACCCCGAGAGTCCGTTGTGCTGCACTGCAAAAAAGC	1020			
QY	1021	TTCCCGCAATTTAGGTAGTAGACACAGAGTCACTCCAATGACCAATGCTAATGCCAGA	1080			
Db	1021	TTCCCGCAATTTAGGTAGTAGACACAGAGTCACTCCAATGACCAATGCTAATGCCAGA	1080			

OY 1081 GCATTTTCGCACTCTGGCCAGTAAACTAATCGAGCTGAGGTTCCCTACCACAGCGAGATC 1140
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| | | | |
Db 1141 TTGGACATAGGCGAGCGCACCGGCTCGTAGAAATGTTTTCCGAGCACAGATATCATTTGTGC 1200
OY 1201 TGCCCCATGCGTAGTCCAGAAAGACCCCGACCCGATGTAATAATCCCGCATAAACTGGCG 1260
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OY 1261 GAAAAAGCGTGCAAGATTACAAACAGAACTTGATGAGAAGATTAAAGATTCTCCGACC 1320
| | | | |
Db 1261 GAAAAAGCGTGCAAGATTACAAACAGAACTTGATGAGAAGATTAAAGATTCTCCGACC 1320
OY 1321 GTACTTGATACGCGCGATGCTGAAAACACCATGCTCTGCTTTCACAACTGTTACCTGC 1380
| | | | |
Db 1321 GTACTTGATACGCGCGATGCTGAAAACACCATGCTCTGCTTTCACAACTGTTACCTGC 1380
OY 1381 AACATGCGTGCGGAATATTCGGTCATGACAGACGTGTATATCAAACGCTCCGGAATATC 1440
| | | | |
Db 1381 AACATGCGTGCGGAATATTCGGTCATGACAGACGTGTATATCAAACGCTCCGGAATATC 1440
OY 1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCCTGTACTGGATTGGCTTCGACACCAACCAG 1500
| | | | |
Db 1441 TATCATCAGGCTATGAAAGGCGTGCGGACCCCTGTACTGGATTGGCTTCGACACCAACCAG 1500
OY 1501 TTCAATGTTCTCGGCTATGGCAGGTTCTGTAACCTGCGTACAAACACCACTGGGCGAGCAG 1560
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Db 1501 TTCAATGTTCTCGGCTATGGCAGGTTCTGTAACCTGCGTACAAACACCACTGGGCGAGCAG 1560
OY 1561 AAAGTCTTGAAGCGCGTAAACATCGGACTTTGAGCACAAAAGCTGAGTGAAGTAGACA 1620
| | | | |
Db 1561 AAAGTCTTGAAGCGCGTAAACATCGGACTTTGAGCACAAAAGCTGAGTGAAGTAGACA 1620
OY 1621 GGAATAATGTGATAATGAGAAAGAGTTGAAGCCCGGTCGCGGTTTATTCTCC 1680
| | | | |
Db 1621 GGAATAATGTGATAATGAGAAAGAGTTGAAGCCCGGTCGCGGTTTATTCTCC 1680
OY 1681 GTAGATCGACACTTTATCCAGAACACAGAGCCAGCTTGACAGAGCTGGCATCTTCATCG 1740
| | | | |
Db 1681 GTAGATCGACACTTTATCCAGAACACAGAGCCAGCTTGACAGAGCTGGCATCTTCATCG 1740
OY 1741 GTGTTCCACTTGAATGGAAGCAGTCGTACACTTGCCGCTGTGATACAGTGTGAGTTGC 1800
| | | | |
Db 1741 GTGTTCCACTTGAATGGAAGCAGTCGTACACTTGCCGCTGTGATACAGTGTGAGTTGC 1800
OY 1801 GAAGGCTACGTAGTGAAGAAATCACCATCAATCCCGGATCACGGGAGAAACCGTGGA 1860
| | | | |
Db 1801 GAAGGCTACGTAGTGAAGAAATCACCATCAATCCCGGATCACGGGAGAAACCGTGGA 1860
OY 1861 TAGCGGTTACACAATAGCGAGGCTTCTGCTATGCAAGTTACTGACACAGTAAAA 1920
| | | | |
Db 1861 TAGCGGTTACACAATAGCGAGGCTTCTGCTATGCAAGTTACTGACACAGTAAAA 1920
OY 1921 GGAGAACGGGTATGCTTCCCTGTGTGACGTTACATCCCGGCCACCATATGCGATCAGATG 1980
| | | | |
Db 1921 GGAGAACGGGTATGCTTCCCTGTGTGACGTTACATCCCGGCCACCATATGCGATCAGATG 1980
OY 1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGACAAAAAATTCTGTTGGGCTC 2040
| | | | |
Db 1981 ACTGGTATAATGGCCACGGATATATCACCTGACGATGACAAAAAATTCTGTTGGGCTC 2040
OY 2041 AACGAGCGAATTGTCTATTAACGCTAGACTTAAGAAACACCAACACCAATGCAAAATTAC 2100
| | | | |
Db 2041 AACGAGCGAATTGTCTATTAACGCTAGACTTAAGAAACACCAACACCAATGCAAAATTAC 2100
OY 2101 CTTCTGCCGATCATAGCACAAAGGTTCAAGCAATGGGCTAAGAGCGCAAGATGATCTT 2160
| | | | |
Db 2101 CTTCTGCCGATCATAGCACAAAGGTTCAAGCAATGGGCTAAGAGCGCAAGATGATCTT 2160

OY 2161 GATAACGAGAAATGCTGGGTACTAGAGACGCAAGCTTACGTAATGCTGCTGTGGCGC 2220
| | | | |
Db 2161 GATAACGAGAAATGCTGGGTACTAGAGACGCAAGCTTACGTAATGCTGCTGTGGCGC 2220
OY 2221 TTTGCACTAAGAAAGTACATTGCTTTATTCGCCACCTGGAACGAGACCTGCGTAAAA 2280
| | | | |
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OY 2281 GTCCAGCCTCTTTTAGCGCTTTTCCCATGTGTCGTCGATGAGACGACCTTTGGCCATG 2340
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Db 2281 GTCCAGCCTCTTTTAGCGCTTTTCCCATGTGTCGTCGATGAGACGACCTTTGGCCATG 2340
OY 2341 TCGCTGAGGAGAAATTGAACCTGGCAATTGCAACCAAGAAAGAGAGAAAACTGCTGCAG 2400
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Db 2341 TCGCTGAGGAGAAATTGAACCTGGCAATTGCAACCAAGAGAGAGAAAACTGCTGCAG 2400
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OY 2461 AGAGCGAGAACTCCGAGAGACATTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
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Db 2461 AGAGCGAGAACTCCGAGAGACATTCCACCATTAGTGGCAGACAAAGGCATCGAGGCA 2520
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Db 2521 GCCGAGAAATTGTCTGCGAAGTGAAGGAGCTCCAGCGGACATCGAGCAGCATTTAGTT 2580
OY 2581 GAAACCCCGCGGCTCACGTAAGATTAATCTCAAGCAATGACCGTATGATCGGACAG 2640
| | | | |
Db 2581 GAAACCCCGCGGCTCACGTAAGATTAATCTCAAGCAATGACCGTATGATCGGACAG 2640
OY 2641 TATATCGTTGTCTCGCCAAACTGTGTCTGAAGAAATGCCAACTCGCACAGCGCACCCG 2700
| | | | |
Db 2641 TATATCGTTGTCTCGCCAAACTGTGTCTGAAGAAATGCCAACTCGCACAGCGCACCCG 2700
OY 2701 CTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAGGAAGTTACGGGTGAA 2760
| | | | |
Db 2701 CTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAGGAAGTTACGGGTGAA 2760
OY 2761 CCATACGACGCTAAAGTACTGATGCCAGAGAGGTGCCGTACCATGCGCAATTCCTA 2820
| | | | |
Db 2761 CCATACGACGCTAAAGTACTGATGCCAGAGAGGTGCCGTACCATGCGCAATTCCTA 2820
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| | | | |
Db 2821 GCACGTAGTGAAGCGCCACGTTAGTGTCAACGAAAGAGGTTGTGAACCGCAAACTA 2880
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| | | | |
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Db 2941 AAGGACAGAGCTTGCAGAAACAGAGTACGTGTTGACGTGGAACAAGACGTTGCGTTAAG 3000
OY 3001 AAGGAAGAGCCTCAAGTCTGTCTCTCGGAGAACTGACCAACCTCCCTATCATGAG 3060
| | | | |
Db 3001 AAGGAAGAGCCTCAAGTCTGTCTCTCGGAGAACTGACCAACCTCCCTATCATGAG 3060
OY 3061 CTAGCTTGGAGGAGCTGAAGACCCGACCTGCGGTCCCGTACAAAGTGAACAATAGGA 3120
| | | | |
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OY 3121 GTGATAGGCACACCGGGGTGCGGCAAGTCACTATTATCAAGTCAACTGTCACGGCACGA 3180
| | | | |
Db 3121 GTGATAGGCACACCGGGGTGCGGCAAGTCACTATTATCAAGTCAACTGTCACGGCACGA 3180
OY 3181 GATCTTGTTACAGCGGAAAGAAAGAAATTTGTGCGAAATTGAGCGCGACGTGCTAAGA 3240
| | | | |
Db 3181 GATCTTGTTACAGCGGAAAGAAAGAAATTTGTGCGAAATTGAGCGCGACGTGCTAAGA 3240
OY 3241 CTGAGGGGTATGCAAGATTACGTGAAGACAGTAGATTGCGTTATGCTCAACGAGATGCCAC 3300
| | | | |

Db 3241 CTGAGGGTATGACATTAAGTGAAGACAGTATTCGGTTATGCTCAACGGATGCCAC 3300
QY 3301 AAAGCCGTAGAAAGTCTGTACGTTGACGAAGCGTTCCGCTGCCACGACGAGACTACTT 3360
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QY 3361 GCCTTGATTGCTATCGTCAGGCCCCCGCAAGAGTAGTACTATGCGGAGACCCCATGCAA 3420
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Db 3901 GGAACCTTTCAGGCTACTATAGAGACTGGGAAAGCTGAACACAGGAAATAATTGCTGCA 3960
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Db 3961 ATAAACAGCCCCCACTCCCCGTCGAATCCGTTCAAGTGAAGACCAAGTTGCTGGCG 4020
QY 4021 AAAGCATTTGAAACCGATACTAGCCACGGCGGATTCGTACTTACCGGTTGCCAGTGAGC 4080
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QY 4141 ATTTGCATTAAAGTTTTCGGCATGACTTGACAAAGCGACTGTTTCTAAACAGAGCATC 4200
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QY 4321 GTGTTCCAGCTAGCTGGGAAGGCGACAACTTGATTGACAGCGGGGAGAACCGAGATT 4380
Db 4321 GTGTTCCAGCTAGCTGGGAAGGCGCGACAACTTGATTGACAGCGGGGAGAACCGAGATT 4380

Db 4381 GTGTTCCAGCTAGCTGGGAAGGCGCACAACTTGATTGACAGCGGGGAGAACCGAGATT 4380
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Db 4381 ATCTCTGACAGCATTAACCTGCTCCCGGTGAACCGCAATCTTCTCACGCCCTTAGTCCC 4440
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Db 4861 GTCTCAAGCAATACAGAAATGTACTGTATTTCCGACCACTAGACAAACAGCCGTACACGG 4920
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Db 4921 CAATTCAACCCCGCACCATCTGAATTGCGTGATTTGCTCCGTATGAGGGTACAAAGAT 4980
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QY 5281 AATGAACATTAACATCAAGTCTGTGCGCATTCACCTGATCTACAGGCATTACGACGCC 5340
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QY 5401 GCGGACGTAAACATCTATTGCTGTGATAAGAGTGAAGAAAGATCGACGCGGCACTC 5460
Db 5401 GCGGACGTAAACATCTATTGCTGTGATAAGAGTGAAGAAAGATCGACGCGGCACTC 5460

OY 5461 CAACTTAAGAGTCTGTAACAGAGCTGAAGATATGAGATCGACGATGATTA 5520
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Db 5461 CAACTTAAGAGTCTGTAACAGAGCTGAAGATATGAGATCGACGATGATTA 5520
OY 5521 GTATGATTCATCCAGACAGTTCCTGAAGGGAAGAAAGGATTCACTACTACAAAGGA 5580
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OY 5581 AAATTGTAATTCGTACTTCGAAAGCACCAATTCCATCAAGCAGCAAAAGACATGGCGAG 5640
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OY 5641 ATAAAGTCTGTCTCCCTAATGACAGGAAAGTAATGAACAACTGTGCTACATATTG 5700
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OY 5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTCCCGTGCACCATTAACCGTCTAGC 5760
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Db 5701 GGTGAGACCATGGAAGCAATCCGCGAAAAGTCCCGTGCACCATTAACCGTCTAGC 5760
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OY 5821 CTTAGAAGCAATAACGTCAAAAGATTACAGTATGCTCCTCCACCCCCCTTCTAAGCAC 5880
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OY 5881 AAAATTAAAGATGTTCAGAAGGTTCAGTGACGAAAGTAGTCTGTTTAATCCGACACT 5940
5881 AAAATTAAAGATGTTCAGAAGGTTCAGTGACGAAAGTAGTCTGTTTAATCCGACACT 5940
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OY 6061 ACCTCGCTTGATGTCAACAGACATCTCACTGGATATGATGACAGTAGCGAAGGCTCACTT 6120
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OY 6121 TTTTCGAGCTTTAGCGGATCGGACAACTCTAATTACTAGTATGACAGTTGTCGTCAGGA 6180
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OY 6181 CCTAGTTCACTAGAGATAGTAGACCGAAGGAGGTGGTGGCTGACGTTCAATGCCGTC 6240
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OY 6241 CAAGAGCTGCCCTATTCCACCGCCAAGGCTAAAGAAAGATGGCCCGCTGGCAGCGCA 6300
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OY 6361 GGGGTATCCATGTCTCCTCGGATCAATTTTCGACGAGAGACGCGCCGCAAGCGGTA 6420
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OY 6421 CAACCCCTGGCAAGGCCCCCAGGATGTGCTTCTTTCCGATCGTTTCCGACGGA 6480
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OY 6481 GAGATTGATGAGCTGAGCCGCAAGTAAGTCCGAACCCGTCCTGTTTGGATCATTT 6540
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OY 6541 GAACCGGCGAAGTGAACCTCAATTATATCGTCCCGATCAGCCGTAATCTTTCCACTACGC 6600
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OY 6661 TACATATTTTCGACGACACAGGCCCTGGGCACTTGCAAAAAGAGTCCGTTCTGCAGAAC 6720
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OY 6781 GACACGTGCAAAAGAGAACAACTCAAACTCAGGTACCAAGTAGATGCCACCGAAGCCAAC 6840
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OY 7021 GTAGCTGTCTTAACAACATATCTGCAATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
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OY 7081 ACTGACGAGTAGCATGCTTACTTGTGATATGTTAGACGAGACAGTGCATGCTGATACT 7140
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OY 7141 GCAACCTTCTGCCCGCTAAGCTTGAAGTTACCGGAAAAACAAGATATAGAGCCCCG 7200
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Db 7561 CACACAGAGAAAGACCGAAAGTACAGTATCAAGCCGCAAGACCCCTGGCGACTGCT 7620
OY 7621 TACTTATGCGGAGTTCAACCGGAATTAGTGCGTAGGCTTACGCGGCTTGTCCAAAC 7680

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QY	7681	ATTCAACACGCTTTTGTACATGTCGGCGGAGGATTTGTATGCAATCATAGCAAGAACCTTC	7740
Db	7681	ATTCAACACGCTTTTGTACATGTCGGCGGAGGATTTGTATGCAATCATAGCAAGAACCTTC	7740
QY	7741	AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTTGCACAAAAAGCCAAAGCAGAC	7800
Db	7741	AAGCAAGGCGACCCGGTACTGGAGACGGATATCGCATCATTTGCACAAAAAGCCAAAGCAGAC	7800
QY	7801	GCTATGGCGTTAACCCGGTCTGATGATCTTGAGGAGCCTGGGTGTGATCAACCACTACTC	7860
Db	7801	GCTATGGCGTTAACCCGGTCTGATGATCTTGAGGAGCCTGGGTGTGATCAACCACTACTC	7860
QY	7861	GACTTGATCGAGTGCCTTTGGAGAAATATCATCCACCATCTACCTACGGGTACTCGT	7920
Db	7861	GACTTGATCGAGTGCCTTTGGAGAAATATCATCCACCATCTACCTACGGGTACTCGT	7920
QY	7921	TTTAAATTCGGGCGATGATGAAATCCGGAATGTTCTCAACTTTTGTCAACAGATT	7980
Db	7921	TTTAAATTCGGGCGATGATGAAATCCGGAATGTTCTCAACTTTTGTCAACAGATT	7980
QY	7981	TTGAATGTCGTTATCGCCAGCAGAGTACTAGAGAGCGGCTTAAACGTCCAGATGTGCA	8040
Db	7981	TTGAATGTCGTTATCGCCAGCAGAGTACTAGAGAGCGGCTTAAACGTCCAGATGTGCA	8040
QY	8041	GCGTTCATTGGCGACGACAACATCATACATGAGTAGTATCTGCACAAAGAAATGGCTGAG	8100
Db	8041	GCGTTCATTGGCGACGACAACATCATACATGAGTAGTATCTGCACAAAGAAATGGCTGAG	8100
QY	8101	AGGTGCGCCACCCTGGCTCAACATGGAGGTTAAGATCATGACGCGAGTCATCGGTGAGAGA	8160
Db	8101	AGGTGCGCCACCCTGGCTCAACATGGAGGTTAAGATCATGACGCGAGTCATCGGTGAGAGA	8160
QY	8161	CCACCTTACTTCTGCGCGGATTTATCTTGCAAGATTGCTTACTTCCACAGCGTGCCGC	8220
Db	8161	CCACCTTACTTCTGCGCGGATTTATCTTGCAAGATTGCTTACTTCCACAGCGTGCCGC	8220
QY	8221	GTCGCGGATCCCTGAAAAGGCTGTTAAGTTGGGTAAACCGCTCCAGCCGACGACGAG	8280
Db	8221	GTCGCGGATCCCTGAAAAGGCTGTTAAGTTGGGTAAACCGCTCCAGCCGACGACGAG	8280
QY	8281	CAAGACGAAGACAGAAAGCGCTCTGCTAGATGAACAAGGCGTGTAGTAGTAGGT	8340
Db	8281	CAAGACGAAGACAGAAAGCGCTCTGCTAGATGAACAAGGCGTGTAGTAGTAGGT	8340
QY	8341	ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCCGTATGAGGTAGACAATATTACACT	8400
Db	8341	ATAACAGGCACTTTAGCAGTGGCCGTGACGACCCCGTATGAGGTAGACAATATTACACT	8400
QY	8401	GTCCTACTGGCATTTGAGAACTTTTGCCCAAGCAAAAGACATTCCAAGCCATCAGAGGG	8460
Db	8401	GTCCTACTGGCATTTGAGAACTTTTGCCCAAGCAAAAGACATTCCAAGCCATCAGAGGG	8460
QY	8461	GAAATTAAGCATCTCTACGGTGTCTTAATAGTCAGCATAGTACATTTCACTGACTAA	8520
Db	8461	GAAATTAAGCATCTCTACGGTGTCTTAATAGTCAGCATAGTACATTTCACTGACTAA	8520
QY	8521	TACTACAACACCAACCACT 8539	
Db	8521	TACTACAACACCAACCACT 8539	

RESULT 3	
AAFB84024	
ID	AAFB84024 standard; cDNA; 11282 BP.
XX	
AC	AAFB84024;
XX	
DT	22-AUG-2001 (first entry)
XX	
DE	Complete cDNA sequence of plasmid pCYTt.

XX		pcytc; cellular; taxol; gene therapy; RNA replication; endogenous gene;
KW		ss.
KX		Synthetic.
OS		WO200142442-A2.
PV		14-JUN-2001.
XX		08-DEC-2000; 2000WO-IB001841.
PF		10-DEC-1999; 99US-0169988P.
PR		(CYTO-) CYTOS BIOTECHNOLOGY AG.
PA		Hennecke F, Renner WA;
PI		WPI, 2001-381672/40.
DR		The invention relates to a method of modifying expression characteristics
XX		of an endogenous target gene within a genome of a eukaryotic cell or
PT		producing a polypeptide encoded by the target gene of a eukaryotic cell.
PT		The method involves inserting exogenous polynucleotides in 5' and 3'
PT		regions flanking the coding region of target gene to produce a
XX		recombinant eukaryotic host cell, and culturing the cell. The method is
PS		useful for producing cells which exhibit increased expression of
CC		endogenous genes which lead to the production of additional products, and
CC		for amplifying endogenous genes involved in the production of cellular
CC		products such as taxol. The method is also useful for producing
CC		biological products, and their derivatives, and for regulating the
CC		activity of target genes by modifying the expression of regulatory
CC		proteins involved in the regulation of the target genes. The method or a
CC		DNA vector system is useful for performing gene therapy on an individual
CC		(e.g., domesticated animal or human). The present sequence represents the
CC		complete cDNA sequence of a vector pcyts, a DNA vector system for
CC		modifying the expression characteristics of an endogenous target gene
CC		within the genome of a eukaryotic cell comprising a 5' targeting
CC		construct and a 3' targeting construct, where the 5' and 3' targeting
CC		construct encode genetic elements required for RNA replication
XX		
Sequence	11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;	
Query Match	100.0%; Score 8539; DB 5; Length 11282;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 8539; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CTGACGGCGCCTGTAGCGGCATTAAGCGCGCGGTGTGTTAGCGCGACGCTGA	60
DB	1 CTGACGGCGCCTGTAGCGGCATTAAAGCGCGCGGTGTGTTAGCGCGACGCTGA	60
QY	61 CCCTACTACCTTGCCAGCGCCCTTAGCGGCCGCTCTTCCTTCCTTCCTTCCTTCG	120
DB	61 CCCTACTACCTTGCCAGCGCCCTTAGCGGCCGCTCTTCCTTCCTTCCTTCCTTCG	120
QY	121 CCACGTTGCGCGCTTCCCCTCAAGCTCTAATCGGGGGCTCCCTTTAGGGTTCGAT	180
DB	121 CCACGTTGCGCGCTTCCCCGTCAGCTCTAATCGGGGGCTCCCTTTAGGGTTCGAT	180
QY	181 TTAGTGCTTTACGGCACCTCGACCCCAAATACTTGATTAGGGTGATGTTCAAGTAGTG	240
DB	181 TTAGTGCTTTACGGCACCTCGACCCCAAATACTTGATTAGGGTGATGTTCAAGTAGTG	240
QY	241 GGCCATCGCCCTGATAGACGGTTTTTTCCGCCCTTTGACGTTGGAGTCCACGTTCTTAATA	300
DB	241 GGCCATCGCCCTGATAGACGGTTTTTTCCGCCCTTTGACGTTGGAGTCCACGTTCTTAATA	300

QY	301	GTGACTCTTGTGCCAACTGGAACAACACTCAACCTATCTCGGTCATTTCTTTGATT	360
Db	301	GTGACTCTTGTGCCAACTGGAACAACACTCAACCTATCTCGGTCATTTCTTTGATT	360
QY	361	TATAAGGATTTTGGCGATTTCGGCCTATTGGTTAAAAATGAGCTGATTTAACAAAAAT	420
Db	361	TATAAGGATTTTGGCGATTTCGGCCTATTGGTTAAAAATGAGCTGATTTAACAAAAAT	420
QY	421	TTAACGCCAATTTTAAACAATAATTAACGCTTACAATTTCCATTTCGCCATTCAAGCTGCG	480
Db	421	TTAACGCCAATTTTAAACAATAATTAACGCTTACAATTTCCATTTCGCCATTCAAGCTGCG	480
QY	481	CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCCTATTACGCCAGCTGGCGAAAG	540
Db	481	CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCCTATTACGCCAGCTGGCGAAAG	540
QY	541	GGGATGTGCTGCAAGCGCATTAAGTTGGGTAACGCCAGGGTTTCCAGTCAAGCAGTTG	600
Db	541	GGGATGTGCTGCAAGCGCATTAAGTTGGGTAACGCCAGGGTTTCCAGTCAAGCAGTTG	600
QY	601	TAAAAAGACGGCCAGTGAAGCGCCCAATTAACCTCACTAAAGGGAACAAAAGCTGGCTAG	660
Db	601	TAAAAAGACGGCCAGTGAAGCGCCCAATTAACCTCACTAAAGGGAACAAAAGCTGGCTAG	660
QY	661	TGGATCCAGTCTTATGCAATACTCTGTAGTCTTGCAACATGTGTAACGATGATTAGCAA	720
Db	661	TGGATCCAGTCTTATGCAATACTCTGTAGTCTTGCAACATGTGTAACGATGATTAGCAA	720
QY	721	CATGCTTACAAAGAGAAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGTAC	780
Db	721	CATGCTTACAAAGAGAAAAAGCACCGTGCATGCCGATTGGTGAAGTAAGTGTAC	780
QY	781	GATCGTGCTTATTAGGAAGCAACAGACGGGTCTGCATGGAATTGGACGAACCACTGAA	840
Db	781	GATCGTGCTTATTAGGAAGCAACAGACGGGTCTGCATGGAATTGGACGAACCACTGAA	840
QY	841	TTCGCGATTGCAGAGATATTGTATTAAAGTGCCCTACCTGATACCGTGCAGATTGACGG	900
Db	841	TTCGCGATTGCAGAGATATTGTATTAAAGTGCCCTACCTGATACCGTGCAGATTGACGG	900
QY	901	CGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCACTACCATCACAATGAGAGAG	960
Db	901	CGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCACTACCATCACAATGAGAGAG	960
QY	961	CCAAGTAGTAACGTAAGACGTAGACCCCCAGAGTCCGTTGTCTGTGCAACTGCAAAAAAGC	1020
Db	961	CCAAGTAGTAACGTAAGACGTAGACCCCCAGAGTCCGTTGTCTGTGCAACTGCAAAAAAGC	1020
QY	1021	TTCCCGCAATTTGAGGTAGTACACAGCAGGTCACTCCAATGACCATGCTAATGCCAGA	1080
Db	1021	TTCCCGCAATTTGAGGTAGTACACAGCAGGTCACTCCAATGACCATGCTAATGCCAGA	1080
QY	1081	GCATTTTCCGATCTGGCCAGTAATACTAATCGAGCTGAGGTTCTACCACAGCAGCATC	1140
Db	1081	GCATTTTCCGATCTGGCCAGTAATACTAATCGAGCTGAGGTTCTACCACAGCAGCATC	1140
QY	1141	TTGGAACATAGGCAGCGCACCGGCTCTGTAATGTTTCCGACCAACAGTATCATTTGTCTC	1200
Db	1141	TTGGAACATAGGCAGCGCACCGGCTCTGTAATGTTTCCGACCAACAGTATCATTTGTCTC	1200
QY	1201	TGCCCATGCGTAGTCCAGAAGACCCGGAACCGCATGATGAATAAGCCAGTAAACTGGCG	1260
Db	1201	TGCCCATGCGTAGTCCAGAAGACCCGGAACCGCATGATGAATAAGCCAGTAAACTGGCG	1260
QY	1261	GAAAAAGCGTGCAAGATTACAAACAAGAACTTGATGAGAAGATTAAAGATCTCCGGAAC	1320
Db	1261	GAAAAAGCGTGCAAGATTACAAACAAGAACTTGATGAGAAGATTAAAGATCTCCGGAAC	1320
QY	1321	GTAATTGATACGCCGGATGCTGAACAACCATCGCTCTGCTTTCAACAAGATGTACCTGC	1380
Db	1321	GTAATTGATACGCCGGATGCTGAACAACCATCGCTCTGCTTTCAACAAGATGTACCTGC	1380
QY	1381	AACATGCGTGCCGAATATTTCCGTCATGCAGGACGCTGTATATCAACGCTCCCGGAATATC	1440

Db	1381	AACATGCGGTGCGGAATATTCCGTCATGACGACGTGTATTATCAACGCTCCCGGAATCATC	1440
QY	1441	TATCATCAGCCTATGAAAGCGTGGGACCCCTGTACTGAAATGGCTTCGACACCAACCAG	1500
Db	1441	TATCATCAGCCTATGAAAGCGCTGGGACCCCTGTACTGAAATGGCTTCGACACCAACCAG	1500
QY	1501	TTTCATGTTCTCGGCTATGGCAGGTTCTGTAACCTGCGGTACAAACCAACTGGGCCGACGAG	1560
Db	1501	TTTCATGTTCTCGGCTATGGCAGGTTCTGTAACCTGCGGTACAAACCAACTGGGCCGACGAG	1560
QY	1561	AAAGTCCTTGAAGCGCGTAACATCGGACTTTTGACGACACAAAGCTGAGTGAAGTTAGACA	1620
Db	1561	AAAGTCCTTGAAGCGCGTAACATCGGACTTTTGACGACACAAAGCTGAGTGAAGTTAGACA	1620
QY	1621	GGAAATTTGTCGATATAGAGAAAGAGTTGAAGCCCGGGTCCGGGTTATTCTCC	1680
Db	1621	GGAAATTTGTCGATATAGAGAAAGAGTTGAAGCCCGGGTCCGGGTTATTCTCC	1680
QY	1681	GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGACAGAGCTGGCATCTTCCATCG	1740
Db	1681	GTAGGATCGACACTTTATCCAGAACACAGAGCCAGCTTGACAGAGCTGGCATCTTCCATCG	1740
QY	1741	GTTGTTCCACTTGAATGAAAGCAGTGTACACTTGCCGCTGTGATACAGTGTGAGTTGC	1800
Db	1741	GTTGTTCCACTTGAATGAAAGCAGTGTACACTTGCCGCTGTGATACAGTGTGAGTTGC	1800
QY	1801	GAAAGCTACGTAGTGAAGAAATCAACATCAGTCCCGGATCAAGGAGAAACCGTGGGA	1860
Db	1801	GAAAGCTACGTAGTGAAGAAATCAACATCAGTCCCGGATCAAGGAGAAACCGTGGGA	1860
QY	1861	TACGCGGTTACACACAAATAGCGAGGCTTCTGCTATGCAAAGTTACTGACACAGTTAAA	1920
Db	1861	TACGCGGTTACACACAAATAGCGAGGCTTCTGCTATGCAAAGTTACTGACACAGTTAAA	1920
QY	1921	GGAGAACGGGTATCGTTCCTGCTGTGACGTACATCCCGGCCACCATATGCGATCAGATG	1980
Db	1921	GGAGAACGGGTATCGTTCCTGCTGTGACGTACATCCCGGCCACCATATGCGATCAGATG	1980
QY	1981	ACTGTATTAATGCCCCACGGATATATCACTGACGATGCACAAAACCTTCTGTTGGGCTC	2040
Db	1981	ACTGTATTAATGCCCCACGGATATATCACTGACGATGCACAAAACCTTCTGTTGGGCTC	2040
QY	2041	AACCAGCGAATTGTCATTAAACGGTAGACTAAACAGAACACCAACCATGCAAAATTAC	2100
Db	2041	AACCAGCGAATTGTCATTAAACGGTAGACTAAACAGAACACCAACCATGCAAAATTAC	2100
QY	2101	CTTCTGCCGATCATTAGCACAAAGGTTACGAAATGGGCTTAAGAGCGCAAGATGATCTT	2160
Db	2101	CTTCTGCCGATCATTAGCACAAAGGTTACGAAATGGGCTTAAGAGCGCAAGATGATCTT	2160
QY	2161	GATAACGAGAAATGCTGGGTACTAGAACCGCAAGCTTACGTAATGCTGCTTGTGGCG	2220
Db	2161	GATAACGAGAAATGCTGGGTACTAGAACCGCAAGCTTACGTAATGCTGCTTGTGGCG	2220
QY	2221	TTTTCGACTAAGAAAGTACATTTCGTTTATCGCCCACTTGGAACGACAGCTGCGTTAAA	2280
Db	2221	TTTTCGACTAAGAAAGTACATTTCGTTTATCGCCCACTTGGAACGACAGCTGCGTTAAA	2280
QY	2281	GTCCAGCCTCTTTAAGCGCTTTTCCATGTGTCGCTATGACGACCTTTTGCCCATG	2340
Db	2281	GTCCAGCCTCTTTAAGCGCTTTTCCATGTGTCGCTATGACGACCTTTTGCCCATG	2340
QY	2341	TCCGTGAGGCAGAAATTGAAACTGGCATTTGCAACCAAGAAGGAGAAAACTGCTGCAG	2400
Db	2341	TCCGTGAGGCAGAAATTGAAACTGGCATTTGCAACCAAGAAGGAGAAAACTGCTGCAG	2400
QY	2401	GTTCTCGAGGAATTAGTCATGAGAGCCAGGCTGCTTTTGAGGATGCTCAGAGGAAGCC	2460
Db	2401	GTTCTCGAGGAATTAGTCATGAGAGCCAGGCTGCTTTTGAGGATGCTCAGAGGAAGCC	2460
QY	2461	AGAGCGAGAAAGCTCCGAGAAAGCACTTCCACCATTTAGTGGCAGCAAAAGGCATCGAGCA	2520
Db	2461	AGAGCGAGAAAGCTCCGAGAAAGCACTTCCACCATTTAGTGGCAGCAAAAGGCATCGAGCA	2520

Db 2461 AGAGCGGAGAACTCCGAGAGCACTTCCACCATTAAGTGGCAGACAAGGCATCGAGCA 2520
QY 2521 GCCGAGAACTTGTCTGCGAAGTGAAGGGCTCCAGGCGGACATCGAGCAGCATTAGTT 2580
Db 2521 GCCGAGAACTTGTCTGCGAAGTGAAGGGCTCCAGGCGGACATCGAGCAGCATTAGTT 2580
QY 2581 GAAACCCCCCGGGTCAAGTAAAGATTAATCTCAAGCAATGACCGTATGATCGGACAG 2640
Db 2581 GAAACCCCCCGGGTCAAGTAAAGATTAATCTCAAGCAATGACCGTATGATCGGACAG 2640
QY 2641 TATATCGTTGTCTCGCCAACTGTGCTGAAGAATGCCAACTCGCACCGCACCCG 2700
Db 2641 TATATCGTTGTCTCGCCAACTGTGCTGAAGAATGCCAACTCGCACCGCACCCG 2700
QY 2701 CTAGCAGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGTACGCGTGCA 2760
Db 2701 CTAGCAGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGTACGCGTGCA 2760
QY 2761 CCATACGAGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
Db 2761 CCATACGAGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAGAATTCCTA 2820
QY 2821 GCACGTAGTGAAGCGCCACGTTAGTTGTAACAACGAAAGAGAGTTGTGAACCGCAACTA 2880
Db 2821 GCACGTAGTGAAGCGCCACGTTAGTTGTAACAACGAAAGAGAGTTGTGAACCGCAACTA 2880
QY 2881 TACCACATTTGCCATGCATGCGCCCGCCAGAATACAGAAGAGAGCAGTACAAGGTTACA 2940
Db 2881 TACCACATTTGCCATGCATGCGCCCGCCAGAATACAGAAGAGAGCAGTACAAGGTTACA 2940
QY 2941 AAGCAGAGCTTGCAGAAACAGAGTACTGTTTGACGTGACAGAAAGCGTTGCGTTAAG 3000
Db 2941 AAGCAGAGCTTGCAGAAACAGAGTACTGTTTGACGTGACAGAAAGCGTTGCGTTAAG 3000
QY 3001 AAGGAAGAGCCTCAGGTCTGCTCTCGGAGAACTGACCAACCTCCCTATCATGAG 3060
Db 3001 AAGGAAGAGCCTCAGGTCTGCTCTCGGAGAACTGACCAACCTCCCTATCATGAG 3060
QY 3061 CTAGCTTGGAGGGAAGTGAAGACCCGACCTGCGGTCCCGTACAAGTCCGAAACATAGCA 3120
Db 3061 CTAGCTTGGAGGGAAGTGAAGACCCGACCTGCGGTCCCGTACAAGTCCGAAACATAGCA 3120
QY 3121 GTGATAGGCACACCGGGGTGCGGCAAGTCACTATTATCAAGTCAACTGTCAAGGACGCA 3180
Db 3121 GTGATAGGCACACCGGGGTGCGGCAAGTCACTATTATCAAGTCAACTGTCAAGGACGCA 3180
QY 3181 GATCTTGTTAACAAGCGGAAAGAAATTTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
Db 3181 GATCTTGTTAACAAGCGGAAAGAAATTTGTCGCGAAATTGAGGCCGACGTGCTAAGA 3240
QY 3241 CTGAGGGGTATGAGATTACGTGGAAGACAGTAGATTGCTTAACGATGCCAC 3300
Db 3241 CTGAGGGGTATGAGATTACGTGGAAGACAGTAGATTGCTTAACGATGCCAC 3300
QY 3301 AAAGCCGTAGAAGTGTGTAAGTGAAGCGTTGCGGTGCGACGACGAGGACACTACTT 3360
Db 3301 AAAGCCGTAGAAGTGTGTAAGTGAAGCGTTGCGGTGCGACGACGAGGACACTACTT 3360
QY 3361 GCCTTGAATTGCTATGCTCAGGCCCCCGCAGAAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
Db 3361 GCCTTGAATTGCTATGCTCAGGCCCCCGCAGAAAGGTAGTACTATGCGGAGACCCCATGCAA 3420
QY 3421 TGGGATTTCTCAACATGATGCAACTAAAGGTACATTTCAATCACTGAAAAAGACATA 3480
Db 3421 TGGGATTTCTCAACATGATGCAACTAAAGGTACATTTCAATCACTGAAAAAGACATA 3480
QY 3481 TGCACCAAGACATTTCTACAAGTATATCTCCGCGTTGCACACAGCCAGTTACAGCTATT 3540
Db 3481 TGCACCAAGACATTTCTACAAGTATATCTCCGCGTTGCACACAGCCAGTTACAGCTATT 3540
QY 3541 GTATGCACTGCATTACGATGGAAGATGAAAAACACGAACCGGTGCAAGAAGAACATT 3600
Db 3541 GTATGCACTGCATTACGATGGAAGATGAAAAACACGAACCGGTGCAAGAAGAACATT 3600

QY 3601 GAAATCGATATTACAGGGGCCCAAAAGCCGAAGCCAGGGGATATCATCTGCATGTTTC 3660
Db 3601 GAAATCGATATTACAGGGGCCCAAAAGCCGAAGCCAGGGGATATCATCTGCATGTTTC 3660
QY 3661 CGCGGTGGGTTAAGCAATTGCAATCGACTATCCCGGACATGAAGTATGACAGCCGCG 3720
Db 3661 CGCGGTGGGTTAAGCAATTGCAATCGACTATCCCGGACATGAAGTATGACAGCCGCG 3720
QY 3721 GCCTCACAAGGGCTAACCAAGAAAGAGTGTATGCTCCGCGCAAAAAGTCAATGAAAAC 3780
Db 3721 GCCTCACAAGGGCTAACCAAGAAAGAGTGTATGCTCCGCGCAAAAAGTCAATGAAAAC 3780
QY 3781 CCACTGTACCGCATCAATCAGACATGTGAACGTGTTGCTCAACCCGACTGAGGACAGG 3840
Db 3781 CCACTGTACCGCATCAATCAGACATGTGAACGTGTTGCTCAACCCGACTGAGGACAGG 3840
QY 3841 CTAGTGTGAAAACTTGCAGGGCGACCCCATGATTAAAGACCCCATTAACATACCTTAA 3900
Db 3841 CTAGTGTGAAAACTTGCAGGGCGACCCCATGATTAAAGACCCCATTAACATACCTTAA 3900
QY 3901 GGAACCTTTCAGGCTACTATAGAAGACTGGGAAGCTGAACAAGGAATATGCTGCA 3960
Db 3901 GGAACCTTTCAGGCTACTATAGAAGACTGGGAAGCTGAACAAGGAATATGCTGCA 3960
QY 3961 ATAAACAGCCCCACTCCCGGTGCCAATCCGTTACGTGCAAGACCAAGCTTGTGCGCG 4020
Db 3961 ATAAACAGCCCCACTCCCGGTGCCAATCCGTTACGTGCAAGACCAAGCTTGTGCGCG 4020
QY 4021 AAAGCATTTGGAACCGATACAGCCACGCGCGGTATCGTACTTACCGGTGCCAGTGAAC 4080
Db 4021 AAAGCATTTGGAACCGATACAGCCACGCGCGGTATCGTACTTACCGGTGCCAGTGAAC 4080
QY 4081 GAACTGTTCCACAGTTTGGGATGACAAACCAATTCGCGCATTTACGCTTAGAGTA 4140
Db 4081 GAACTGTTCCACAGTTTGGGATGACAAACCAATTCGCGCATTTACGCTTAGAGTA 4140
QY 4141 ATTTGATTTAAGTTTTCGCGATGAGCTTGACAAAGCGAAGCTGTTTCTAAACAGAGCATC 4200
Db 4141 ATTTGATTTAAGTTTTCGCGATGAGCTTGACAAAGCGAAGCTGTTTCTAAACAGAGCATC 4200
QY 4201 CCACTAACGTACCATCCCGCGATTTCAGCGAGCGCGGTAGCTCATTTGGACAACAGCCCA 4260
Db 4201 CCACTAACGTACCATCCCGCGATTTCAGCGAGCGCGGTAGCTCATTTGGACAACAGCCCA 4260
QY 4261 GGAACCCGCAAGTATGGGTACGATCACGCCCATTTGCCGCGAAGCTCTCCCGTAGATTCCG 4320
Db 4261 GGAACCCGCAAGTATGGGTACGATCACGCCCATTTGCCGCGAAGCTCTCCCGTAGATTCCG 4320
QY 4321 GTGTTCCAGCTAGCTGGGAAGGCAACAACTTGATTGCAAGCGGGAGAACCAAGATT 4380
Db 4321 GTGTTCCAGCTAGCTGGGAAGGCAACAACTTGATTGCAAGCGGGAGAACCAAGATT 4380
QY 4381 ATCTTGACACAGCATAACTGGTCCCGGTGAACCGCAATCTTCTCACGCGCTTAGTCCCC 4440
Db 4381 ATCTTGACACAGCATAACTGGTCCCGGTGAACCGCAATCTTCTCACGCGCTTAGTCCCC 4440
QY 4441 GAGTACAAGAGAAAGCAACCCGCGCGGTCAAAAAATTTCTGAACCAAGTTCAAAACCAAC 4500
Db 4441 GAGTACAAGAGAAAGCAACCCGCGCGGTCAAAAAATTTCTGAACCAAGTTCAAAACCAAC 4500
QY 4501 TCAGTACTTGTGTATCAGAGAAAAATTTGAAGTCCCGTAAAGAAATCGAAATGATC 4560
Db 4501 TCAGTACTTGTGTATCAGAGAAAAATTTGAAGTCCCGTAAAGAAATCGAAATGATC 4560
QY 4561 GCCCCGATTGGCATAGCCCGGTGACAGATAAGAACTAACCTGCTTTCGGGTTTCGCGCG 4620
Db 4561 GCCCCGATTGGCATAGCCCGGTGACAGATAAGAACTAACCTGCTTTCGGGTTTCGCGCG 4620
QY 4621 CAGGCAAGGTACGACCTGGTGTTCATCAACATTTGGAATAAATACAGAAAACCAACCTTT 4680
Db 4621 CAGGCAAGGTACGACCTGGTGTTCATCAACATTTGGAATAAATACAGAAAACCAACCTTT 4680

OY		4681	CAGCAGTGCGAAGACCATGCGGGCACTTTAAAAACCCCTTTTCGGCTTCGGCCCTGAATTGT 	4740
Db		4681	CAGCAGTGCGAAGACCATGCGGGCACTTTAAAAACCCCTTTTCGGCTTCGGCCCTGAATTGT 	4740
OY		4741	TTAAACTCAGGAGCACCTCGTGTGAAGTCCATGGCTACGCCGACAAGTAGAG 	4800
Db		4741	TTAAACTCAGGAGCACCCCTCGTGTGAAGTCCATGGCTACGCCGACAAGTAGAG 	4800
OY		4801	GACGTAGTCACCGCTCTTGCCAGAAGTTTGTCAAGGTCTGACGGAGACCAATTGT 	4860
Db		4801	GACGTAGTCACCGCTCTTGCCAGAAGTTTGTCAAGGTCTGACGGAGACCAATTGT 	4860
OY		4861	GTTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAATAAGAACAGCCGTACACGG 	4920
Db		4861	GTTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAATAAGAACAGCCGTACACGG 	4920
OY		4921	CAATTCACCCCGCAACCATCTGAATTGCGTATTTGTCGGTATGAGGGTACAAGAT 	4980
Db		4921	CAATTCACCCCGCAACCATCTGAATTGCGTATTTGTCGGTATGAGGGTACAAGAT 	4980
OY		4981	GGAGTTGGAGCCGCGCGCTCATACCCGACCAAAGGAGAAATTGCTGACTGTCAAGAG 	5040
Db		4981	GGAGTTGGAGCCGCGCGCTCATACCCGACCAAAGGAGAAATTGCTGACTGTCAAGAG 	5040
OY		5041	GAAAGCAGTTGTCAACGCAAGCCAATCCGCTGGGTAGACCAAGCGAAGAGTCTGCCGTGCC 	5100
Db		5041	GAAAGCAGTTGTCAACGCAAGCCAATCCGCTGGGTAGACCAAGCGAAGAGTCTGCCGTGCC 	5100
OY		5101	ATCTATAAACGTTGGCCGACAGTTTACCATTACGCCAGGAGACAGCACCGCAGAG 	5160
Db		5101	ATCTATAAACGTTGGCCGACAGTTTACCATTACGCCAGGAGACAGCACCGCAGAG 	5160
OY		5161	ATGACTGTGTGCTAGGAAGAAGTAGATCCACGCGGTGCGCCCTGATTTCCGGAAGCAC 	5220
Db		5161	ATGACTGTGTGCTAGGAAGAAGTAGATCCACGCGGTGCGCCCTGATTTCCGGAAGCAC 	5220
OY		5221	CCAGAAAGCAGAAAGCCTTGAAAATTGCTACAAAAAGCCTACCATGCAAGTGACAGCTTAAGTA 	5280
Db		5221	CCAGAAAGCAGAAAGCCTTGAAAATTGCTACAAAAAGCCTACCATGCAAGTGACAGCTTAAGTA 	5280
OY		5281	AATGAACATTAACATCAAGTCTGTGCGCCATTCCACTGCTATCTACAGGCATTTACGCAACC 	5340
Db		5281	AATGAACATTAACATCAAGTCTGTGCGCCATTCCACTGCTATCTACAGGCATTTACGCAACC 	5340
OY		5341	GGAAAAAGACCGCCTTGAAGTATCACTTAATCTGCTTGACAAACCGCCTAGACAGAACTGAC 	5400
Db		5341	GGAAAAAGACCGCCTTGAAGTATCACTTAATCTGCTTGACAAACCGCCTAGACAGAACTGAC 	5400
OY		5401	GCGGACGTAACCATCTATTGCTGEGATAAGAAAGTGAAAGAAAGATCGACGCGGCACTC 	5460
Db		5401	GCGGACGTAACCATCTATTGCTGEGATAAGAAAGTGAAAGAAAGATCGACGCGGCACTC 	5460
OY		5461	CAACTTAAGAGTCTGTAACAGAGCTGAAGAGATGAAGATATGAGAGATCGACGATGATTAA 	5520
Db		5461	CAACTTAAGAGTCTGTAACAGAGCTGAAGAGATGAAGATATGAGAGATCGACGATGATTAA 	5520
OY		5521	GTAATGATTCATCCAGACAGTTGCTTGAAAGGGAAGAAAGGATTCAGTACTACAAAAAGGA 	5580
Db		5521	GTAATGATTCATCCAGACAGTTGCTTGAAAGGGAAGAAAGGATTCAGTACTACAAAAAGGA 	5580
OY		5581	AAATGTATTCTGTAATTCGAAGGCACCAAATTCATCAAGCAGCAAAAGACATGCGCGAG 	5640
Db		5581	AAATGTATTCTGTAATTCGAAGGCACCAAATTCATCAAGCAGCAAAAGACATGCGCGAG 	5640
OY		5641	ATAAAGGTCTGTTCCCTTAATGACCAAGAAAGTAATGAACAATGCTGTGCTACATATTG 	5700
Db		5641	ATAAAGGTCTGTTCCCTTAATGACCAAGAAAGTAATGAACAATGCTGTGCTACATATTG 	5700
OY		5701	GGTGAGACCATGGAAGCAATCCGCGAAGAAAGTGCCCGGTGCAACCATTAACCCGTGCTTAAGC 	5760
Db		5701	GGTGAGACCATGGAAGCAATCCGCGAAGAAAGTGCCCGGTGCAACCATTAACCCGTGCTTAAGC 	5760
OY		5761	CCGCCCCAAAACGTTGCCGTGCTTTGCATGTATGCCATGACGCCAGAAAGGCTCCACAGA 	5820

Db	5761	CCGCCCCAAACGTTGCCGTGCCTTTGCATGTATGCCATGACGCCAGAAAGGGTCCACAGA	5820
QY	5821	CTTAGAAGCAATAACTCAAGAAGTTACAGTATGCTCTCCACCCCCCTTCTTAAGCAC	5880
Db	5821	CTTAGAAGCAATAACTCAAGAAGTTACAGTATGCTCTCCACCCCCCTTCTTAAGCAC	5880
QY	5881	AAAAATTAAGAAATGTTCAGAAGGTTCAAGTGCACGAAAGTAGTCTGTTTAATCCGACACT	5940
Db	5881	AAAAATTAAGAAATGTTCAGAAGGTTCAAGTGCACGAAAGTAGTCTGTTTAATCCGACACT	5940
QY	5941	CCCGCATTCGTTCCCGCCCCGTAAGTACATAGAAGTCCAGAAACAGCCCTACCGCTCCTCT	6000
Db	5941	CCCGCATTCGTTCCCGCCCCGTAAGTACATAGAAGTCCAGAAACAGCCCTACCGCTCCTCT	6000
QY	6001	GCACAGGCCGAGAGAGGCCCCCCGAAGTTGTAGCCACACCGTCACCATCTACAGCTGATTAAC	6060
Db	6001	GCACAGGCCGAGAGAGGCCCCCCGAAGTTGTAGCCACACCGTCACCATCTACAGCTGATTAAC	6060
QY	6061	ACCTCGCTTGATGTCAAGACATCTCACTGATATGATGACAGTAGCGAAGGCTCACTT	6120
Db	6061	ACCTCGCTTGATGTCAAGACATCTCACTGATATGATGACAGTAGCGAAGGCTCACTT	6120
QY	6121	TTTTGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGACAGTTGGTCGTCAGGA	6180
Db	6121	TTTTGAGCTTTAGCGGATCGGACAACTCTATTACTAGTATGACAGTTGGTCGTCAGGA	6180
QY	6181	CCTAGTTCACTAGAGATAGTAGACCGAAGGCAAGTGTGTGCTGACGTTCAATGCCGTC	6240
Db	6181	CCTAGTTCACTAGAGATAGTAGACCGAAGGCAAGTGTGTGCTGACGTTCAATGCCGTC	6240
QY	6241	CAAGAGCCTGCCCTATTCCACCGCCCAAGGCTAAAGAAAGATGGCCCCGCTGCGACGGCA	6300
Db	6241	CAAGAGCCTGCCCTATTCCACCGCCCAAGGCTAAAGAAAGATGGCCCCGCTGCGACGGCA	6300
QY	6301	AGAAAAGAGCCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTTTTGGT	6360
Db	6301	AGAAAAGAGCCCCACTCCACCGGCAAGCAATAGCTCTGAGTCCCTCCACCTCTTTTGGT	6360
QY	6361	GGGGTATCCATGTCTCCCTCCGGATCAATTTTCGACGGAGAGACGGCCCCGACAGCGGTA	6420
Db	6361	GGGGTATCCATGTCTCCCTCCGGATCAATTTTCGACGGAGAGACGGCCCCGACAGCGGTA	6420
QY	6421	CAACCCCTGGCAACAGGCCCCACGGATGTGCTATGCTTTCCGATCGTTTCCGACGGA	6480
Db	6421	CAACCCCTGGCAACAGGCCCCACGGATGTGCTATGCTTTCCGATCGTTTCCGACGGA	6480
QY	6481	GAGATTGATGAGCTGAGCCGACAGAGTAACCTGAGTCCGAACCCGCTCCTGTTTGATCATTT	6540
Db	6481	GAGATTGATGAGCTGAGCCGACAGAGTAACCTGAGTCCGAACCCGCTCCTGTTTGATCATTT	6540
QY	6541	GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC	6600
Db	6541	GAACCGGGCGAAGTGAACTCAATTATATCGTCCCGATCAGCCGTATCTTTTCCACTACGC	6600
QY	6601	AAGCAGAGACGTAGACGACAGAGCAGAGGACTGAATACTGACTAACCGGGGTAGGTGGG	6660
Db	6601	AAGCAGAGACGTAGACGACAGAGCAGAGGACTGAATACTGACTAACCGGGGTAGGTGGG	6660
QY	6661	TACATATTTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAGTCCGTTCTGCAGAAC	6720
Db	6661	TACATATTTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAGAGTCCGTTCTGCAGAAC	6720
QY	6721	CAGCTTACAGAACCGACCTTGGAGCGCAATGTCTGGAAAAGAAATTCAATGCCCGGTGCTC	6780
Db	6721	CAGCTTACAGAACCGACCTTGGAGCGCAATGTCTGGAAAAGAAATTCAATGCCCGGTGCTC	6780
QY	6781	GACACGTCGAAAAGAGAACTCAAACTCAGGTACCAAGATGATGCCACCGAAGCCAAAC	6840
Db	6781	GACACGTCGAAAAGAGAACTCAAACTCAGGTACCAAGATGATGCCACCGAAGCCAAAC	6840
QY	6841	AAAAGTAGTACCACTCTGTAAGTAGAAAATCAGAAAAGCCATTAACCACTGACGACTA	6900
Db	6841	AAAAGTAGTACCACTCTGTAAGTAGAAAATCAGAAAAGCCATTAACCACTGACGACTA	6900

Db 6841 AAAAGTAGTACCACTCTCGTAAAGTAGAATAACAGAAAGCCATAACCACTGAGCGACTA 6900
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Db 6901 CTGTACGACTACGACTGTATATACTCTGCCACAGATCAGCCAGAAATGCTATAGATCACC 6960
QY 6961 TATCCGAAACCATTTGTAATCTCCAGTAGCCGTACCCGCCAACTACTCCGATCCACAGTTGCT 7020
Db 6961 TATCCGAAACCATTTGTAATCTCCAGTAGCCGTACCCGCCAACTACTCCGATCCACAGTTGCT 7020
QY 7021 GTAGCTGTCTGTAACTAATACTCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
Db 7021 GTAGCTGTCTGTAACTAATACTCTGCATGAGAACTATCCGACAGTAGCATCTTATCAGATT 7080
QY 7081 ACTGACGAGTACGATGCTTAATCTTGATATGTTAGACGAGACAGTCCGATGCTGATACT 7140
Db 7081 ACTGACGAGTACGATGCTTAATCTTGATATGTTAGACGAGACAGTCCGATGCTGATACT 7140
QY 7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATAGAGCCCCG 7200
Db 7141 GCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATAGAGCCCCG 7200
QY 7201 AATATCCGCAAGTCCGCTTCCATCAGCGATGCAACAACGCTACAAAATGCTCATTTGCC 7260
Db 7201 AATATCCGCAAGTCCGCTTCCATCAGCGATGCAACAACGCTACAAAATGCTCATTTGCC 7260
QY 7261 GCAACTAAAGAAATTTGCAACGTCACGACAGTGCCTGAATGCTCCACAAGCTCAGCG 7320
Db 7261 GCAACTAAAGAAATTTGCAACGTCACGACAGTGCCTGAATGCTCCACAAGCTCAGCG 7320
QY 7321 ACATTCAATGTCGAATGCTTTGAAAAATATGATGTATAGACGATTTGGAGAGATTG 7380
Db 7321 ACATTCAATGTCGAATGCTTTGAAAAATATGATGTATAGACGATTTGGAGAGATTG 7380
QY 7381 GCTCGAAGCCAAATTAGATTACCACTGATGTTGTACCCGATATGAGCTAGACTGAAA 7440
Db 7381 GCTCGAAGCCAAATTAGATTACCACTGATGTTGTGTACCCGATATGAGCTAGACTGAAA 7440
QY 7441 GGCCCTAAGGCGCGCCACTATTGCAAAAGCGTATAATTGTTGCTCCATTGCAAGAAGTG 7500
Db 7441 GGCCCTAAGGCGCGCCACTATTGCAAAAGCGTATAATTGTTGCTCCATTGCAAGAAGTG 7500
QY 7501 CCTATGATAGATTCTCATGACATGAAAGAGACGCTGAAAGTTACCAAGGCAAGAAA 7560
Db 7501 CCTATGATAGATTCTCATGACATGAAAGAGACGCTGAAAGTTACCAAGGCAAGAAA 7560
QY 7561 CACACAGAAAGAAAGCCGAAAGTACAAAGTACAAAGCCGCAAGAAACCTGGCGACTGCT 7620
Db 7561 CACACAGAAAGAAAGCCGAAAGTACAAAGTACAAAGCCGCAAGAAACCTGGCGACTGCT 7620
QY 7621 TACTTAATGCGGATTCACCCGGAATTAGTGCCTAGGCTTACCGCCGCTTGTCCAAAC 7680
Db 7621 TACTTAATGCGGATTCACCCGGAATTAGTGCCTAGGCTTACCGCCGCTTGTCCAAAC 7680
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Db 7681 ATTACACAGCTTTTGAACATGTCGCGGAGGATTTTGATGCAATCATAGACAGAACTTC 7740
QY 7741 AAGCAAGGCGAAGCCGCTACTGAGACGGAATATCGCATATTCGACAAAAGCCAAAGACGAC 7800
Db 7741 AAGCAAGGCGAAGCCGCTACTGAGACGGAATATCGCATATTCGACAAAAGCCAAAGACGAC 7800
QY 7801 GCTATGCGCTTAAACCGCTGTATGATCTTTGAGAGACCTGGGTGTGATCAACCACTACTC 7860
Db 7801 GCTATGCGCTTAAACCGCTGTATGATCTTTGAGAGACCTGGGTGTGATCAACCACTACTC 7860
QY 7861 GACTTGATGAGTGCCTTTGAGAGAAATATCATCCACCCATCTAAGCGGTACTCGT 7920
Db 7861 GACTTGATGAGTGCCTTTGAGAGAAATATCATCCACCCATCTAAGCGGTACTCGT 7920
QY 7921 TTAAATTCGGGGCGATGATGAATCCGGAATGTTCTCTACACATTTTGTCAACACAGTT 7980
Db 7921 TTAAATTCGGGGCGATGATGAATCCGGAATGTTCTCTACACATTTTGTCAACACAGTT 7980

QY 7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAAAGTCCAGATGTGCA 8040
Db 7981 TTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAAAGTCCAGATGTGCA 8040
QY 8041 GCGTCAATTTGGCGAGCAGCAACATCATACATGAGTAGTATCTGACAAAGAAATGCTGAG 8100
Db 8041 GCGTCAATTTGGCGAGCAGCAACATCATACATGAGTAGTATCTGACAAAGAAATGCTGAG 8100
QY 8101 AGGTGCGCCACCTGGCTCAACATGAGAGGTTAAGATCATGACCGACATCGGTGAGAGA 8160
Db 8101 AGGTGCGCCACCTGGCTCAACATGAGAGGTTAAGATCATGACCGACATCGGTGAGAGA 8160
QY 8161 CCACCTTACTTCTGCGCGGATTTATCTTGCAAGATTGCTTACTCCACAGCGTCCGC 8220
Db 8161 CCACCTTACTTCTGCGCGGATTTATCTTGCAAGATTGCTTACTCCACAGCGTCCGC 8220
QY 8221 GTGGCGGATCCCTGAAAAAGCTGTTAAGTTGGTTAAACCGCTCCAGCGCAGCAGAG 8280
Db 8221 GTGGCGGATCCCTGAAAAAGCTGTTAAGTTGGTTAAACCGCTCCAGCGCAGCAGAG 8280
QY 8281 CAAGACGAAGACAGAAGCGCTCTGCTAGATGAACAAGCGGTGTTAGTAGGT 8340
Db 8281 CAAGACGAAGACAGAAGCGCTCTGCTAGATGAACAAGCGGTGTTAGTAGGT 8340
QY 8341 ATACAGGCACTTTAGCAGTGGCCGTGACGACCCCGGTATGAGGTAGACATATTACACT 8400
Db 8341 ATACAGGCACTTTAGCAGTGGCCGTGACGACCCCGGTATGAGGTAGACATATTACACT 8400
QY 8401 GTCTTACTGGCATTTGAGAACTTTTGCCCAAGAGCAAAAGACATTCCAAAGCATGAGAGG 8460
Db 8401 GTCTTACTGGCATTTGAGAACTTTTGCCCAAGAGCAAAAGACATTCCAAAGCATGAGAGG 8460
QY 8461 GAAATTAAGCATCTCTACGCTGCTCTAAATAGTACGATAGTACATTTTCATCTGACTAA 8520
Db 8461 GAAATTAAGCATCTCTACGCTGCTCTAAATAGTACGATAGTACATTTTCATCTGACTAA 8520
QY 8521 TACTACAACACCAACCACT 8539
Db 8521 TACTACAACACCAACCACT 8539

RESULT 4
ADL71889
ID ADL71889 standard; cDNA; 11282 BP.
XX
AC ADL71889;
XX
DT 20-MAY-2004 (first entry)
XX
DE Temperature inducible alphavirus vector pCytS.
XX
KW Gene expression; vector; pCytS; ss.
OS Rous sarcoma virus.
OS Alphavirus.
OS Chimeric.
PN WO2004018506-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
XX 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX

PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.

PS Example 1; SEQ ID NO 1; 112pp; English.

XX
CC The present sequence is that of the tightly regulated temperature
CC inducible alphavirus expression system pCytTS containing a Rous sarcoma
CC virus (RSV) promoter. The vector can be used to drive transcription of
CC mRNA from a nucleic acid molecule of the invention. A claimed nucleic
CC acid molecule comprises: (A) a first polynucleotide element which encodes
CC an RNA molecule comprising (a) at least one cis-acting sequence element,
CC (b) a first nucleotide sequence comprising a first open reading frame,
CC the first open reading frame having a nucleotide sequence encoding an RNA
CC -dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, i.e. the cis-acting replication origin oriP and the cis- or trans-
CC acting gene product EBNA-1 with pCytTS ADL71909-ADL71910. Due to the
CC presence of OriP and EBNA-1, the novel vector is maintained episomally in
CC the form of several DNA copies in cell nuclei. These multiple DNA copies
CC may be transcribed from the RSV promoter into CytTS RNA replicons, but
CC remain inactive unless cells are shifted to a certain temperature. Only
CC after temperature induction does replicon replication occur, followed by
CC RNA accumulation and translation in the cell cytoplasm, and production of
CC the polypeptide of interest.

XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 12; Length 11282;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACGCGCCCTGTAGCGCGGCATTAGCGCGCGGTGTGTGTTACCGCGACGCGTGA 60
DB 1 CTGACGCGCCCTGTAGCGCGGCATTAGCGCGCGGTGTGTGTTACCGCGACGCGTGA 60
QY 61 CCGCTACACTTGCAGCGCGCCCTAGCGCGCGCTTCTTCTTCTTCTTCTTCTG 120
DB 61 CCGCTACACTTGCAGCGCGCCCTAGCGCGCGCTTCTTCTTCTTCTTCTTCTG 120
QY 121 CCACGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTAGGGTCCGAT 180
DB 121 CCACGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTAGGGTCCGAT 180
QY 181 TTAGTGTCTTACGCGACCTCGACCCCAAAAACCTGATTAGGTGATGTTCAAGTAGTG 240
DB 181 TTAGTGTCTTACGCGACCTCGACCCCAAAAACCTGATTAGGTGATGTTCAAGTAGTG 240
QY 241 GGCCATCGCCCTGATAGACGGTTTTTCCGCTTTGACGTTGGAGTCCACGTTCTTAATA 300
DB 241 GGCCATCGCCCTGATAGACGGTTTTTCCGCTTTGACGTTGGAGTCCACGTTCTTAATA 300
QY 301 GTGACTCTTGTTCCTCAAACTGGAACAACACTCAATCTCGTCTATCTTTTGTGATT 360
DB 301 GTGACTCTTGTTCCTCAAACTGGAACAACACTCAATCTCGTCTATCTTTTGTGATT 360
QY 361 TATAAGGATTTGCGGATTTGCGCTATGTTAAAAATGAGCTGATTAACAAAAAT 420
DB 361 TATAAGGATTTGCGGATTTGCGCTATGTTAAAAATGAGCTGATTAACAAAAAT 420
QY 421 TTAACGGAATTTTAACAAAATATTAACGCTTAAATTTCCATTCGCCATTGAGCTGCG 480
DB 421 TTAACGGAATTTTAACAAAATATTAACGCTTAAATTTCCATTCGCCATTGAGCTGCG 480

DB 421 TTAACGGAATTTTAACAAAATATTAACGCTTAAATTTCCATTCGCCATTGAGCTGCG 480
QY 481 CAACTGTGGGAAGCGCGATCGGTGCGGCTCTTGGCTATTACGCCAGCTGGCGAAAG 540
DB 481 CAACTGTGGGAAGCGCGATCGGTGCGGCTCTTGGCTATTACGCCAGCTGGCGAAAG 540
QY 541 GGGATGTGCTGCAAGCGGATTAAGTTGGTTAACGCCAGGCTTTCCAGTCACGACGTTG 600
DB 541 GGGATGTGCTGCAAGCGGATTAAGTTGGTTAACGCCAGGCTTTCCAGTCACGACGTTG 600
QY 601 TAAAACGACGCGCAGTGAGCGCGCAATTAACCTCACTTAAGGGAACAAAGCTGCTAG 660
DB 601 TAAAACGACGCGCAGTGAGCGCGCAATTAACCTCACTTAAGGGAACAAAGCTGCTAG 660
QY 661 TGGATCCAGTCTTATGCAATACCTTGTAGTCTTGCAACATGTTAGCAATGAGTTAGCAA 720
DB 661 TGGATCCAGTCTTATGCAATACCTTGTAGTCTTGCAACATGTTAGCAATGAGTTAGCAA 720
QY 721 CATGCTTACAGAGAGAGAAAAAGCACCGTGCAATGCCGATTGGTGAAGTAAGTGCTAC 780
DB 721 CATGCTTACAGAGAGAGAAAAAGCACCGTGCAATGCCGATTGGTGAAGTAAGTGCTAC 780
QY 781 GATCGTCTTATTAAGGAGGCAACAGCGGCTGACATGATGATGAGCAACCACTGAA 840
DB 781 GATCGTCTTATTAAGGAGGCAACAGCGGCTGACATGATGATGAGCAACCACTGAA 840
QY 841 TTCCGATTTGCAAGATATTGTATTAAAGTCCCTACCTGATACCGTGAGATTGACGG 900
DB 841 TTCCGATTTGCAAGATATTGTATTAAAGTCCCTACCTGATACCGTGAGATTGACGG 900
QY 901 CGTAGTACACTATTGAATCAAAACAGCGCAATTTGCACTACCAATCAATGAGAGAG 960
DB 901 CGTAGTACACTATTGAATCAAAACAGCGCAATTTGCACTACCAATCAATGAGAGAG 960
QY 961 CCAGTAGTAACGTAGACGTAGACCCCGCAGAGTCCGTTGTGCTGCACTGCAAAAAAGC 1020
DB 961 CCAGTAGTAACGTAGACGTAGACCCCGCAGAGTCCGTTGTGCTGCACTGCAAAAAAGC 1020
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DB 1021 TTCCCGCAATTTGAGGTAGTAGACACAGAGTCACTCCAAATGACCATGCTAATGCCAGA 1080
QY 1081 GCATTTTTCGCACTCTGCGCAGTAACCTAAATCGAGCTGAGGTTCTTACACAGCAGATC 1140
DB 1081 GCATTTTTCGCACTCTGCGCAGTAACCTAAATCGAGCTGAGGTTCTTACACAGCAGATC 1140
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DB 1141 TTGACATAGGACGCGCACCGGCTCGTAGAATGTTTCCGAGCACGATATCATTTGTGTC 1200
QY 1201 TGCCCATGCGTAGTCCAGAAAGACCCGACCCGATGATGAATACGCCAGTAACTGGCG 1260
DB 1201 TGCCCATGCGTAGTCCAGAAAGACCCGACCCGATGATGAATACGCCAGTAACTGGCG 1260
QY 1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTGTCATGAGAAAGATTAAAGATCTCCGAGAC 1320
DB 1261 GAAAAAGCGTGCAAGATTACAAACAAGAACTGTCATGAGAAAGATTAAAGATCTCCGAGAC 1320
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DB 1321 GTACTTGATAGCGCGGATGCTGAACACCATGCTCTGCTTACAAAGATGTTACCTGC 1380
QY 1381 AACATGCGTGCGGAATATTCCGTATGACGAGCTGTATATCAACGCTCCCGGAATATC 1440
DB 1381 AACATGCGTGCGGAATATTCCGTATGACGAGCTGTATATCAACGCTCCCGGAATATC 1440
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DB 1441 TATCATCAGGCTATGAAAGCGTGCGGACCTGTACTGATTGGCTTGAACACCAACCCAG 1500
QY 1501 TTGATGTTCTGCGCTATGCGAGGTTGTAACCTGCTGACAAACCAACCTGGGCCGAGAG 1560
DB 1501 TTGATGTTCTGCGCTATGCGAGGTTGTAACCTGCTGACAAACCAACCTGGGCCGAGAG 1560

QY 1561 AAAGTCCTGGAAGCGGTAACATCGACTTTGACACACAAAGCTGAGTGAAGGTAGACA 1620
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Db 1561 AAAGTCCTGGAAGCGGTAACATCGACTTTGACACACAAAGCTGAGTGAAGGTAGACA 1620
QY 1621 GGAATAATTGTCGATATGAGGAAGAAGAGTTGAAGCCCGGGTCGGGGTTATTCTCC 1680
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Db 1621 GGAATAATTGTCGATATGAGGAAGAAGAGTTGAAGCCCGGGTCGGGGTTATTCTCC 1680
QY 1681 GTAGGATCGACACTTATCCAGAACACAGAGCCAGCTTGACAGAGCTGGCATCTCCATCG 1740
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Db 1681 GTAGGATCGACACTTATCCAGAACACAGAGCCAGCTTGACAGAGCTGGCATCTCCATCG 1740
QY 1741 GTGTTCCACTTGAATGGAAGCAGTCTGACACTTGCCTGTGATACAGTGTGAGTTGC 1800
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Db 1741 GTGTTCCACTTGAATGGAAGCAGTCTGACACTTGCCTGTGATACAGTGTGAGTTGC 1800
QY 1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGATCACGGGAGAAACCGTGGGA 1860
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Db 1801 GAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGATCACGGGAGAAACCGTGGGA 1860
QY 1861 TACGCGGTACACACAATAGCGAGGCTTCTGCTATGCAAAAGTTACTGACACAGTAAAA 1920
| | | | |
Db 1861 TACGCGGTACACACAATAGCGAGGCTTCTGCTATGCAAAAGTTACTGACACAGTAAAA 1920
QY 1921 GGAGAACGGGTATCGTCCCTGTGTGACAGTATCCCGCCACCATATGCGATCAGATG 1980
| | | | |
Db 1921 GGAGAACGGGTATCGTCCCTGTGTGACAGTATCCCGCCACCATATGCGATCAGATG 1980
QY 1981 ACTGTATAATGGCCACGATATATCACCTGACGATGACACAAAACTTCTGTTGGCTC 2040
| | | | |
Db 1981 ACTGTATAATGGCCACGATATATCACCTGACGATGACACAAAACTTCTGTTGGCTC 2040
QY 2041 AACCAGCGAATTGTCATTAACGCTAGACTAACAGAACACCAACCATGCAAAATTAC 2100
| | | | |
Db 2041 AACCAGCGAATTGTCATTAACGCTAGACTAACAGAACACCAACCATGCAAAATTAC 2100
QY 2101 CTTCTGCCGATCATAGCACAAAGGTTCAAGCAATGGGCTAAGGAGCGCAAGATGATCTT 2160
| | | | |
Db 2101 CTTCTGCCGATCATAGCACAAAGGTTCAAGCAATGGGCTAAGGAGCGCAAGATGATCTT 2160
QY 2161 GATTAACGAGAAAAATGCTGGGTACTAGAGAACGCAAGCTTACGATGCGTGTGGCG 2220
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Db 2161 GATTAACGAGAAAAATGCTGGGTACTAGAGAACGCAAGCTTACGATGCGTGTGGCG 2220
QY 2221 TTTCCGACTAAGAAAGTACATTGTTTATGCGCCCACTGGAACGAGACCTGCGTAAAA 2280
| | | | |
Db 2221 TTTCCGACTAAGAAAGTACATTGTTTATGCGCCCACTGGAACGAGACCTGCGTAAAA 2280
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Db 2341 TCGCTGAGGCGAATAATTGAAACTGGCATTGCAACCAAGAGAGAAAAAACTGCTGAC 2400
QY 2401 GTCTCGAGAGAAATTAGTCATGAGGCGCAAGGCTGCTTTGAGGATGCTCAGAGGAAGCC 2460
| | | | |
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QY 2461 AGAGCGGAGAAAGCTCCGAGAAAGCATTCCACATTAGTGGCAGACAAAGGCATCGAGCA 2520
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| | | | |
Db 2521 GCCGCAAGAGTTGCTGCGAAGTGAAGGGCTCCAGGCGGACATCGAGCAGCATTAATT 2580
QY 2581 GAAACCCCGCGGCTCACGTAAGGATATACTCAAGCAAAATGACCGTATGATCGGACAG 2640
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QY 2641 TATATCGTTGTCCTGCCAAACTCTGTGCTGGAAGATGCCAACTCGCACACGCGCACCCG 2700
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QY 2701 CTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAAGAAAGTACGCGGTGAA 2760
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QY 2761 CCATACGACGCTAAAGTACTGATGCCCAGAGAGGTGCGGTACCATGGCCAGAATTCCTA 2820
| | | | |
Db 2761 CCATACGACGCTAAAGTACTGATGCCCAGAGAGGTGCGGTACCATGGCCAGAATTCCTA 2820
QY 2821 GCACTGAGTGAAGCGCCACGTTAGTGTACAAAGAAAGAGTTTGTGAACCGCAACTA 2880
| | | | |
Db 2821 GCACTGAGTGAAGCGCCACGTTAGTGTACAAAGAAAGAGTTTGTGAACCGCAACTA 2880
QY 2881 TACCACTTGCATGATGCGCCCGCCCAAGATACAGAAAGAGAGCAGTACAGAGTTTACA 2940
| | | | |
Db 2881 TACCACTTGCATGATGCGCCCGCCCAAGATACAGAAAGAGAGCAGTACAGAGTTTACA 2940
QY 2941 AAGCAGAGCTTGACAGAAACAGATACGTGTTTGAACGTGGACAAAGCGTTGCGTTAAG 3000
| | | | |
Db 2941 AAGCAGAGCTTGACAGAAACAGATACGTGTTTGAACGTGGACAAAGCGTTGCGTTAAG 3000
QY 3001 AAGGAGAAAGCCTCAGGCTGCTGCTCTCGGGAGAACTGACCAACCTCCCTATCATAG 3060
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Oy      8521 TACTACACACCAACCACT 8539
Db      8521 TACTACACACCAACCACT 8539
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RESULT 5
ADL71890
ID ADL71890 standard; cDNA; 13068 BP.
XX
AC ADL71890;
XX
DT 20-MAY-2004 (first entry)
XX
DE Temperature inducible alphavirus vector pCyt2s2.1.
XX
KM Gene expression; vector; pCyt2s2.1; ss.
XX
OS Cytomegalovirus.
OS Alphavirus.
OS Chimeric.
XX
PN WO2004018506-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX
PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 1; SEQ ID NO 2; 112bp; English.
XX
CC The present sequence is that of the tightly regulated temperature
CC inducible alphavirus expression system pCyt2s2.1 containing a
CC cytomegalovirus (CMV). The vector can be used to drive transcription of
CC mRNA from a nucleic acid molecule of the invention. A claimed nucleic
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acid molecule comprises: (A) a first polynucleotide element which encodes an RNA molecule comprising (a) at least one cis-acting sequence element, (b) a first nucleotide sequence comprising a first open reading frame, the first open reading frame having a nucleotide sequence encoding an RNA-dependent RNA polymerase, and (c) at least one second nucleotide sequence comprising (i) a second open reading frame (S1) encoding a polypeptide, (ii) a nucleotide sequence complementary to all or a part of the second open reading frame (S1) and (iii) a nucleotide sequence encoding an untranslated RNA molecule or its complement, where the second nucleotide sequence is operably linked to a promoter which is recognised by the RNA-dependent RNA polymerase; (B) a second polynucleotide element comprising an origin of replication; and (C) a third polynucleotide element encoding a replication initiation factor capable of recognising the origin of replication. The nucleic acid molecule, expression systems and vector systems of the invention allow the production of polypeptides and untranslated RNA molecules in host cells. In a specific embodiment, the invention includes the combination of a herpesvirus mini-replicon unit, i.e. the cis-acting replication origin oriP and the cis- or trans-acting gene product EBNA-1 with pCytS. Due to the presence of OriP and EBNA-1, the novel vector is maintained episomally in the form of several DNA copies in cell nuclei. These multiple DNA copies may be transcribed from the CMV promoter into CytS2.1 RNA replicons, but remain inactive unless cells are shifted to a certain temperature. Only after temperature induction does replicon replication occur, followed by RNA accumulation and translation in the cell cytoplasm, and production of the polypeptide of interest.

Sequence 13068 BP; 3555 A; 3379 C; 3204 G; 2930 T; 0 U; 0 Other;

Query Match 89.7%; Score 7657.2; DB 12; Length 13068;

Best Local Similarity 99.9%; Pred. No. 0; Matches 7642; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Oy      893 ATTGACGGCGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCACTACCATCACA 952
Db      869 ATTGACGGCGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCACTACCATCACA 928
Oy      953 TGGAGAGCCAGTAGTAACGTAGACAGACCCAGAGTCCGTTTGTGTCGAAGTGC 1012
Db      929 TGGAGAGCCAGTAGTAACGTAGACAGACCCAGAGTCCGTTTGTGTCGAAGTGC 988
Oy      1013 AAAAAAGCTTCCCGCAATTTGAGGTAGTACACAGCAGGTCACTCCAAATGACCATGCTA 1072
Db      989 AAAAAAGCTTCCCGCAATTTGAGGTAGTACACAGCAGGTCACTCCAAATGACCATGCTA 1048
Oy      1073 ATGCCAGAGCAATTTTCGATCTGGCCAGTAACTAATCGAGCTGAGGTTCTTACCACAG 1132
Db      1049 ATGCCAGAGCAATTTTCGATCTGGCCAGTAACTAATCGAGCTGAGGTTCTTACCACAG 1108
Oy      1133 CGAGCATCTTGACATAGGACGCGACCGCTGTAGAAATGTTTCCGAGCACCATGATC 1192
Db      1109 CGAGCATCTTGACATAGGACGCGACCGCTGTAGAAATGTTTCCGAGCACCATGATC 1168
Oy      1193 ATTGTGTCGCCCATGCGTAGTCCAGAGACCCGACCGCATGATGAATAAGCCAGTA 1252
Db      1169 ATTGTGTCGCCCATGCGTAGTCCAGAGACCCGACCGCATGATGAATAAGCCAGTA 1228
Oy      1253 AACTGGCGGAAAAAGCGTGCAAGATTACAACAAGAACTTGATGAGAGATTAAAGATC 1312
Db      1229 AACTGGCGGAAAAAGCGTGCAAGATTACAACAAGAACTTGATGAGAGATTAAAGATC 1288
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Db      1289 TCCGACCGTACTTGATAGCGCCGATGCTGAAAACCATCGCTCTGCTTTTCAACAAGATG 1348
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Db      1349 TTACCTGCAACATGCGTCCGAAATATTCGTCATGAGGACGTGTATATCAACGCTCCCG 1408
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Db      1409 GAACTATCTATCATCAGGCTATGAAAAGCGTCCGACCTGTACTGATGATTGCTTGACA 1468
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Db 7289 ACTCAGGACATTCATATGCGAATGCTTTCGAAAATATGATGTATAGACGAGTATTGGG 7348
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Db 7349 AGGAGTTGCTCGGAAAGCAATTAGGATTACCACCTGAGTTTGTACCCGATATGTAGCTA 7408
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QY 7433 GACTGAAAGGCCCTAAGCGCCCGCACTATTTGCAAGAAGCTATAATTGGTCCCATTTGC 7492
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Db 7469 AAGAAAGTCCATGATGATGATTCGTCAATGACATGAAAAGAGACGTGAAGTTTACACAG 7528
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Db 7529 GCAAGAAACACACAGAAAGAAAGACCGAAAGTACAAAGTCAAGCCGAGAACCCCTGG 7588
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QY 7613 CGACTGCTTACTTATGCGGGATTCAACGGGAATTAGTCGTAGGCTTACGGCGTCTTGC 7672
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Qy 8153 GTGAGAGCACCTTACTTCTGCGCGGATTTATCTTGCAAGATTGCGTTACTTCCACAG 8212
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Db 8429 TCAGAGGGGAATAAAGCATCTCTACGGTGTCTTAATAGTCAGCATAGTACATTTTCAT 8488
Qy 8513 CTGACTAATACTACACACACCACCCT 8539
Db 8489 CTGACTAATACTACACACACCACCCT 8515

RESULT 6

ADL71909
ID ADL71909 standard; cDNA; 15081 BP.

AC ADL71909;
XX 20-MAY-2004 (first entry)
XX Expression vector pCytTs-Orip.
DE
XX
KW Gene expression; vector; pCytTs; ss.
XX
OS Alphavirus.
OS Human herpesvirus 4.
OS Chimeric.
XX
PN WO2004018506-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX
PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 2; SEQ ID NO 21; 112pp; English.
XX
CC The present sequence is that of expression vector pCytTs-Orip. A claimed

CC nucleic acid molecule comprises: (A) a first polynucleotide element which
CC encodes an RNA molecule comprising (a) at least one cis-acting sequence
CC element, (b) a first nucleotide sequence comprising a first open reading
CC frame, the first open reading frame having a nucleotide sequence encoding
CC an RNA-dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, e.g. the cis-acting replication origin orip from Epstein Barr
CC virus, with pCysts ADL71889, creating pCytTs-Orip. Due to the presence of
CC Orip, the novel vector is maintained episomally in the form of several
CC DNA copies in cell nuclei. These multiple DNA copies may be transcribed
CC from a Rous sarcoma virus or cytomegalovirus promoter into pCysts RNA
CC replicons, but remain inactive unless cells are shifted to a certain
CC temperature. Only after temperature induction does replicon replication
CC occur, followed by RNA accumulation and translation in the cell
CC cytoplasm, and production of the polypeptide of interest.

XX
SQ Sequence 15081 BP; 4101 A; 3826 C; 3676 G; 3478 T; 0 U; 0 Other;

Query Match 89.7%; Score 7657.2; DB 12; Length 15081;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7642; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 893 ATTGACGGCGTAGTACACACTATTGATCAAAACAGCCGACCAATTGCACTACCATCACAA 952
Db 869 ATTGACGGCGTAGTACACACTATTGATCAAAACAGCCGACCAATTGCACTACCATCACAA 928
Qy 953 TGAGAGGCCAGTAGTAACGCTAGACGAGACCCCGAGAGTCCGTTTGTGTCGAACCTGC 1012
Db 929 TGAGAGGCCAGTAGTAACGCTAGACGAGACCCCGAGAGTCCGTTTGTGTCGAACCTGC 988
Qy 1013 AAAAAAGCTTCCCGCAATTGAGGTAGTAGACACAGCAGGTCACTCCAAATGACCATGCTA 1072
Db 989 AAAAAAGCTTCCCGCAATTGAGGTAGTAGACACAGCAGGTCACTCCAAATGACCATGCTA 1048
Qy 1073 ATGCCAGAGCATTTTGCATCTGGCCAGTAACCTAATCGAGCTGGAGGTTCTTACCACAG 1132
Db 1049 ATGCCAGAGCATTTTGCATCTGGCCAGTAACCTAATCGAGCTGGAGGTTCTTACCACAG 1108
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Db 1109 CGACGATCTTGACATAGGACGCGACCGGCTGTAGAAATGTTTTCGAGCACACAGTATC 1168
Qy 1193 ATTGTGTGCCCCCATGCGTAGTCCAGAAAGACCCGACCGCATGATGAATAGCCAGTA 1252
Db 1169 ATTGTGTGCCCCCATGCGTAGTCCAGAAAGACCCGACCGCATGATGAATAGCCAGTA 1228
Qy 1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAGATTAAAGATC 1312
Db 1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAGATTAAAGATC 1288
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Db 1349 TTACCTGCAACATGCGTGCCGAATATTCGTCATGACGACGTTATATCAACGCTCCCG 1408
Qy 1433 GAACATATCATCATCAGGCTATGAAGGCGTGCGGACCTGTACTGGAATTGGCTTGACA 1492
Db 1409 GAACATATCATCATCAGGCTATGAAGGCGTGCGGACCTGTACTGGAATTGGCTTGACA 1468

QY 1493 CCACCCAGTTCATGTTCTCGGCTATGCGAGGTTGCTACCCCTGCGTACAACACCACTGGG 1552
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Db 1469 CCACCCAGTTCATGTTCTCGGCTATGCGAGGTTGCTACCCCTGCGTACAACACCACTGGG 1528
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Db 1529 CCGACGAGAAAGTCCCTTGAGCGCGGTACATCGGACTTTGCAAGCAAAAGCTGAGTGAAG 1588
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Db 1889 CAGTAAAGAGAAACGGGTATCGTTCCCTGTGTGCACAGTACATCCGGGCCACCATATGCG 1948
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QY 1973 ATCAGATGACTGTATATATGCGCACGGAATATATCACCTGACGATGCACAAAAACCTTCTGG 2032
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Db 2009 TTGGGCTCAACGAGGAATGTCAATTAACGGTAGAGACTAACGAGAAACCAACCATATGC 2068
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Db 2069 AAAATTACTTCTGCCGATCATAGCAACAAGGTTCAAGCAATGGGCTAAGAGCGCAAGG 2128
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QY 2333 TGCCCATGTGCTGAGGCAAGAAATGAAACTGGCATTGCAACCAAGAGAGAAAAAC 2392
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QY 2633 TCGACAGTATATCGTTGTTCTCGCCAAACTCTGTGCTGAAGAAATGCCAAACTCGCACAG 2692
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QY 2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAGGAAGTACG 2752
| | | | |
Db 2669 CGCACCCGCTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAGGAAGTACG 2728
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QY 2753 CCGTCCGAACCATACGACGCTAAAGTACTGATGCCAGAGAGGTGCCGTACCATGGCCAG 2812
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Db 3389 CCATGCAATGCGGATTTCTCAACATGATGCAACTAAAGGTACATTCAATCACCTGAAA 3448
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QY 3473 AAGACATATGACCAAGACATTCTCAAGTATATCTCCCGCGCTTGACACAGCCAGTTA 3532
| | | | |
Db 3449 AAGACATATGACCAAGACATTCTCAAGTATATCTCCCGCGCTTGACACAGCCAGTTA 3508
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| | | | |
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| | | | |
Db 3569 AGAACATTGAATCGATATTACAGAGGGCCACAAAGCCGAAGCCAGGGGATATCATCTGTA 3628
| | | | |
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| | | | |

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QY 4793 ACAGTGAGAGCTAGTCAACCGCTCTTGCCAGAAAAATTGTGACGGGTGTCTGCAGCGAGAC 4852
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Db 5429 CGGCACTCCAATTAAAGAGTCTGTAAACAGAGCTGAAGGATGAAGATATGAGATTCGACG 5488
QY 5513 ATGAGTTAGTATGATTCATCCAGACAGTTGCTGAAGGAAAGGAAAGGATTCAGTACTA 5572
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Db 5609 TGGCGGAGATTAAGGTCTGTTCCTTAATGACCAAGAAAGTATGAACAACCTGTGTGCT 5668
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Db 7949 ACACAGTTTGAATGTCTTATCGCCAGCAGAGTACTGAAGAAGCGGCTTAAAGCTCCA 8008
| | | | |
QY 8033 GATGTGAGCGGTTCAATGGCGACGACAAACATCATGAGTAGTATCTGACAAAGAAA 8092
| | | | |

Db 8009 GATGTGACGCTTCATTGGCGACGACAAACATCATATGAGTAGTATCTGACAAAGAA 8068
QY 8093 TGGCTGAGAGGTGGCCACCTGGCTCAACATGAGGTTAAGATCATCGACGAGTCATCG 8152
Db 8069 TGGCTGAGAGGTGGCCACCTGGCTCAACATGAGGTTAAGATCATCGACGAGTCATCG 8128
QY 8153 GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGAAGATTCGGTTACTTCCACAG 8212
Db 8129 GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGAAGATTCGGTTACTTCCACAG 8188
QY 8213 CGTGGCCGCTGGCGGATCCCTGAAAAGGCTGTTAAGTTGGTTAAACCGCTCCAGCCG 8272
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QY 8453 TCAGAGGGGAATAAGCATCTCTACGGTGGTCTTAATAAGTCAGCATAGTACATTTTCAT 8512
Db 8429 TCAGAGGGGAATAAGCATCTCTACGGTGGTCTTAATAAGTCAGCATAGTACATTTTCAT 8488

QY 8513 CTGACTAATACTACACACCAACCACT 8539
Db 8489 CTGACTAATACTACACACCAACCACT 8515

RESULT 7
ADL71910
ID ADL71910 standard; cDNA; 17753 BP.

XX AC ADL71910;
XX DT 20-MAY-2004 (first entry)

XX DE Expression vector pCytTs-OPE.

XX KM Gene expression; vector; pCytTs; ss.

XX OS Alphavirus.

OS Human herpesvirus 4.

OS Chimeric.

XX PN WO2004018506-A2.

PD 04-MAR-2004

XX PF 21-AUG-2003; 2003WO-EP009291.

XX PR 22-AUG-2002; 2002US-0404928P.

XX PR 11-DEC-2002; 2002US-0432259P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PI Ivanova L, Renner WA, Saudan P;

XX DR WI; 2004-226795/21.

XX PT New nucleic acid molecule comprising first, second and third

XX PT polynucleotide elements, useful for regulating the expression of a

XX PT polypeptide or an untranslated RNA molecule.

XX PS Example 2; SEQ ID NO 22; 112pp; English.

XX CC The present sequence is that of expression vector pCytTs-OPE. A claimed

CC nucleic acid molecule comprises: (A) a first polynucleotide element which
CC encodes an RNA molecule comprising (a) at least one cis-acting sequence
CC element, (b) a first nucleotide sequence comprising a first open reading
CC frame, the first open reading frame having a nucleotide sequence encoding
CC an RNA-dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, e.g. the cis-acting replication origin orip and replication
CC initiation factor EBNA1 from Epstein Barr virus, with pCytTs ADL71889,
CC creating pCytTs-ORE. Due to the presence of Orip and EBNA1, the novel
CC vector is maintained episomally in the form of several DNA copies in cell
CC nuclei. These multiple DNA copies may be transcribed from a Rous sarcoma
CC virus or cytomegalovirus promoter into pCytTs RNA replicons, but remain
CC inactive unless cells are shifted to a certain temperature. Only after
CC temperature induction does replicon replication occur, followed by RNA
CC accumulation and translation in the cell cytoplasm, and production of the
CC polypeptide of interest.

XX SQ Sequence 17753 BP; 4502 A; 4902 C; 4209 G; 4140 T; 0 U; 0 Other;

Query Match: 89.7%; Score 7657.2; DB 12; Length 17753;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7642; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 893 ATTGACGGCGTAGTACACACTATTGAATCAACAGCCGACCAATTGCACTACCATCACAA 952
Db 869 ATTGACGGCGTAGTACACACTATTGAATCAACAGCCGACCAATTGCACTACCATCACAA 928

QY 953 TGGAGAAAGCCAGTAGTAACGTAAGCAGTACAGCCCGAGAGTCCGTTGCTGCAACTGC 1012
Db 929 TGGAGAAAGCCAGTAGTAACGTAAGCAGTACAGCCCGAGAGTCCGTTGCTGCAACTGC 988

QY 1013 AAAAAAGCTTCCGCAATTTGAGGTAGTACAGACAGAGTCACTCCAAATGACCATGCTA 1072
Db 989 AAAAAAGCTTCCGCAATTTGAGGTAGTACAGACAGAGTCACTCCAAATGACCATGCTA 1048

QY 1073 ATGCCAGAGCAATTTCCGATCTGGCCAGTAACATAATCGAGCTGAGGTTCCACACAG 1132
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Db 1109 CGAGATCTTGACATAGGACAGCGCACCGGCTGTAGATGTTTCCGAGCACCAATATC 1168

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Db 1289 TCCGACCGTACTTGATACGCCGATGCTGAACACCATCGCTGCTTTCACAACGATG 1348

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Db 1349 TTACCTGCAACATGCGTCCGGAATATTCGTCATGCAAGAGCTGTATATCAACGCTCCG 1408

QY 1433 GAACTATCTATCATCAGGCTATGAAGGCGTGGGACCTGTACTGATGGCTTGACA 1492
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Qy 3713 CAGCCGCGGCTCACAAGGGCTAACCAAGAAAGAGTGTATGCCGCGCAAAAAGTCA 3772
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Qy 4073 AGTGAGCGCACTGTTCACACAGTTTCCGAGTGAACAACCATTCGGGCCATTACGCCCT 4132
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Db 4289 GATTTCGCGTGTTCAGCTAGCTGGGAAGGGACAACAATTGATTTGACACGGGGAGAA 4348
Qy 4373 CCAGAGTTATCTTGCAACGATTAACCTGTCGCGGTGAACCGCAATCTTCTCAGCGCT 4432
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QY 5873 CTAAGCACAAAATTAAAGATGTTCAAGAGGTTCAGTGCACGAAAAGTAGTCTGTTTAATC 5932
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 QY 5933 CGCACACTCCCGCATTCGTTCCCGCCCGTAGTACATAGAAGTGCCAGAACGCTACCG 5992
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 QY 5993 CTCCTCTGCA CAGGCCGAGAGAGGCCCGGAAGTTGTAGCGACACCGTCAACCATCTACAG 6052
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 QY 6053 CTGATAACACTCGCTTGATGTACAGACATCTCACTGGATATGGATGACAGTAGCGAAG 6112
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 Db 6089 GCTCACTTTTTTCGAGCTTTAGCGGATCGACAACTCTATTACTAGTATGGACAGTTGGT 6148
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 QY 6413 CAGCGGTACAA CCCCCTGGCAACAGGCCCA CGGATGTGCTATGTCTTTCGGATCGTTT 6472
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 QY 6473 CCGACGGAGAGATTGATGAGCTGAGCCGAGAGTAAGTCCGAA CCGTCTGTTG 6532
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 Db 6449 CCGACGGAGAGATTGATGAGCTGAGCCGAGAGTAAGTCCGAA CCGTCTGTTG 6508
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 QY 6593 CACTACGACAGACAGACGTAAGCGACGAGACAGAGAGACTGAATACTGACTAACCCGGG 6652
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 Db 6569 CTTTACGACAGACAGACGTAAGCGACGAGACAGAGAGACTGAATACTGACTAACCCGGG 6628
 QY 6653 TAGGTGGGTACATATTTTCGACCGGACACAGGCCCTGGGCACTTGCAGAAAAGAGTCCGTTT 6712
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 QY 6833 AAGCCAACAAAAGTAGGTACCACTCTCGTAAAGTAGAANAATCAGAAAGCCATACCACTG 6892
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 QY 6893 AGCGACTACTGTCAAGGACTACGACTGTATTAATCTTGCCA CAGATCAGCCAGAAATGCTATA 6952
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 QY 7013 AGTTGGCTGTAGCTGTCTGTAAACAATATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
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 Db 6989 AGTTGGCTGTAGCTGTCTGTAAACAATATCTGCATGAGAACTATCCGACAGTAGCATCTT 7048
 QY 7073 ATCAGATTACTGACGAGTAGCATGCTTACTTGGATATGGTAGACGAGACAGTCCGATGCC 7132
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 QY 7133 TGGATTCTGCAACCTTCTGCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATA 7192
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 QY 7253 TCATTGCCGCACTAAAGAAATTGCAACGTCA CGCAGATGCGTGAACCTGCCACACTGG 7312
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 QY 7313 ACTCAGCGACATTCAATGTGGAATGCTTTGAAAATATGCA TGTATGACGAGTATTGGG 7372
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 QY 7553 GCACGAAACACACAGAGAAGAACCCGAAAGTCAAGTGAATCAAGCCGCAAGAACCCCTGG 7612
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 QY 8033 GATGTGCAAGCGTTCA TTGCGACGACAACATCATACATGGAGTAGTATCTGACAAAAGAA 8092


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Db 8069 TGGCTGAGAGGTGCGCCACCTGGCTCAACATGAGGTTAAGATCATGACGAGTCATCG 8128
Qy 8153 GTGAGAGCAACCTTACTTCTGCGCGGATTATCTTGCAAGATTGCTTACTTCCACAG 8212
Db 8129 GTGAGAGCAACCTTACTTCTGCGCGGATTATCTTGCAAGATTGCTTACTTCCACAG 8188
Qy 8213 CGTCCCGCGTGGCGGATCCCTGAAAAGCTTTTAAGTTGGGTAAACCGCTCCACGCCG 8272
Db 8189 CGTCCCGCGTGGCGGATCCCTGAAAAGCTTTTAAGTTGGGTAAACCGCTCCACGCCG 8248
Qy 8273 ACCAGCAGCAAGACGAAAGACGAGACGCGCTCTGCTAGATGAAACAAAGCGGTGTTA 8332
Db 8249 ACCAGCAGCAAGACGAAAGACGAGACGCGCTCTGCTAGATGAAACAAAGCGGTGTTA 8308
Qy 8333 GAGTAGGTATTAACAGGCACTTTAGCAGTGGCGGTGACGACCCGTTAGGTAGACATA 8392
Db 8309 GAGTAGGTATTAACAGGCACTTTAGCAGTGGCGGTGACGACCCGTTAGGTAGACATA 8368
Qy 8393 TTACACCTGTCTACTGCGCATTTGAGAACTTTGCCAGAGCAAAAGAGATTCCAAAGCA 8452
Db 8369 TTACACCTGTCTACTGCGCATTTGAGAACTTTGCCAGAGCAAAAGAGATTCCAAAGCA 8428
Qy 8453 TCAGAGGGGAAATAAAGCATCTCTACGGTGTCTTAATAGTCAAGCATGATTTTCAAT 8512
Db 8429 TCAGAGGGGAAATAAAGCATCTCTACGGTGTCTTAATAGTCAAGCATGATTTTCAAT 8488
Qy 8513 CTGACTAATATCAACACCAACCACCT 8539
Db 8489 CTGACTAATATCAACACCAACCACCT 8515
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RESULT 8
AAK77354
ID AAK77354 standard; DNA; 9951 BP.
XX
AC AAK77354;
XX
DT 09-AUG-1999 (first entry)
XX
DE Polynucleotide sequence of psinRep 5.
XX
KW Nucleic acid identification; exogenous protein; gene sorting;
KM growth factor; membrane receptor; sindbis virus; ss.
XX
OS Synthetic.
XX
PN WO925876-A1.
XX
PD 27-MAY-1999.
XX
PF 17-NOV-1998; 98WO-US024520.
XX
PR 17-NOV-1997; 97US-00972218.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
PI Bailey JE, Renner WA, Orberger GH, Koller D;
XX
DR WPI; 1999-357620/30.
XX
PT Isolating genes encoding proteins with selected properties, useful for
PT identifying therapeutic agents or targets.
XX
PS Disclosure; Fig 11A-C; 136pp; English.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing a population of eukaryotic host cells, culturing the
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cells under suitable conditions and identifying cells that contain the recombinant nucleic acid. The method is used to sort genes according to the type of proteins they express, and also to identify new ligand/receptor interactions. Typical applications of the nucleic acid and the exogenous protein are in isolation of new growth factors, cytokines, membrane receptors, cytoplasmic, organelle or nuclear proteins, all of which may be useful as therapeutic agents or therapeutic targets, e.g. apoptosis-promoting or tumour suppressing proteins, regulators of cell proliferation or metabolic processes etc. The protein can also be used to screen for specific modulators. The nucleic acid can also be used as sources of therapeutic antisense or ribozyme sequences. The method allows the protein (rather than a partial DNA sequence) to be isolated and, since a wide range of cells can be used, they can be expressed with the correct glycosylation pattern

Sequence 9951 BP; 2852 A; 2461 C; 2464 G; 2174 T; 0 U; 0 Other;

Query Match	89.4%	Score 7637.4;	DB 2;	Length 9951;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 7641;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
Qy 893 ATTGACGGCGTAGTACACACTATTGAATCAACAGCCGACCAATTGCACTACATCACAA 952				
Db 1 ATTGACGGCGTAGTACACACTATTGAATCAACAGCCGACCAATTGCACTACATCACAA 60				
Qy 953 TGGAGAGCCAGTAGTAACGTAGACGTAGACCCCCAGAGTCCGTTGCTGCAACTGC 1012				
Db 61 TGGAGAGCCAGTAGTAACGTAGACGTAGACCCCCAGAGTCCGTTGCTGCAACTGC 120				
Qy 1013 AAAAAAGCTTCCCGCAATTGAGGTAGTAGACACAGCAGGTCACTCCAAATGACCATGCTA 1072				
Db 121 AAAAAAGCTTCCCGCAATTGAGGTAGTAGACACAGCAGGTCACTCCAAATGACCATGCTA 180				
Qy 1073 ATGCCAGAGCAATTTTCGCATCTGGCCAGTAACTAATCGAGCTGGAGTTCTTACCACAG 1132				
Db 181 ATGCCAGAGCAATTTTCGCATCTGGCCAGTAACTAATCGAGCTGGAGTTCTTACCACAG 240				
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Db 241 CGACGATCTTGACATAGGACGCGACCGGCTGTAGAAATGTTTCCGAGCACCAAGTATC 300				
Qy 1193 ATTGTGTGCCCCATGCGTAGTCCAGAAAGCCCGACCGCATGATGAATAGCCAGTA 1252				
Db 301 ATTGTGTGCCCCATGCGTAGTCCAGAAAGCCCGACCGCATGATGAATAGCCAGTA 360				
Qy 1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGATGAGAAATTAAGATC 1312				
Db 361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGATGAGAAATTAAGATC 420				
Qy 1313 TCCGACCGTACTTGATAGCGCCGATGCTGAACAACCATGCTCTGCTTCAACAAGATG 1372				
Db 421 TCCGACCGTACTTGATAGCGCCGATGCTGAACAACCATGCTCTGCTTCAACAAGATG 480				
Qy 1373 TTACCTGCAACATGCGTCCGAATATTCGTCATGACGAGCGTGTATCAACGCTCCCG 1432				
Db 481 TTACCTGCAACATGCGTCCGAATATTCGTCATGACGAGCGTGTATCAACGCTCCCG 540				
Qy 1433 GAACATCTATCATCAGGCTATGAAGGCGTGCGGACCCCTGTACTGATTGGCTTCGACA 1492				
Db 541 GAACATCTATCATCAGGCTATGAAGGCGTGCGGACCCCTGTACTGATTGGCTTCGACA 600				
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Db 601 CCACCCAGTTTCAATGTTCTCGGCTATGCGCAGGTTGTAACCTGCTACACCAACTGGG 660				
Qy 1553 CCGACGAGAAAGTCTTGAAGCGCGTAACTCGGACTTTGACAGACAAAGCTGAGTGAAG 1612				
Db 661 CCGACGAGAAAGTCTTGAAGCGCGTAACTCGGACTTTGACAGACAAAGCTGAGTGAAG 720				
Qy 1613 GTAGACAGAAATTTGCGATATGAGAGAGAGGTTGAAGCCCGGCTCGCGGTTT 1672				
Db 721 GTAGACAGAAATTTGCGATATGAGAGAGAGGTTGAAGCCCGGCTCGCGGTTT 780				

OY 1673 ATTTCTCCGTAGATCGACACTTTATCCAGAACACAGAGCCAGCTTGAGAGCTGCGATC 1732
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OY 1733 TTCCATCGGTTTCCACTTGAATGGAAGCAGTCGTACACTTGGCGTGTGATACAGTGG 1792
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OY 1973 ATCAGATGACTGTATATATGCGCACGGAATATACACCTGACGATGACAAAACCTTGG 2032
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OY 2333 TGCCCATGTGCTGAGGCAAGAAATTGAACTGGCATTGCAACCAAGAGAGGAAAAAC 2392
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OY 2393 TGCTGCAGGCTCGAGGAATTAGTCATGAGGCGCAAGGCTGCTTTGAGGATGCTCAGG 2452
|||||
Db 1501 TGCTGCAGGCTCGAGGAATTAGTCATGAGGCGCAAGGCTGCTTTGAGGATGCTCAGG 1560
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OY 2513 TCGAGGCAAGCCAGAGAAAGTTGTCTGCGAAGTGAGAGGGCTCCAGCGGACATCGAGCAG 2572
|||||
Db 1621 TCGAGGCAAGCCAGAGAAAGTTGTCTGCGAAGTGAGAGGGCTCCAGCGGACATCGAGCAG 1680
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OY 2813 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTAACAAGAAAGAGGTTGTGAACC 2872
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Db 1921 AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTAACAAGAAAGAGTTGTGAACC 1980
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|||||
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Db 3001 TACCTAAAGAAACTTTCAGGCTACTATAGAGACTGGGAAGCTGAACACAAGGAATAA 3060
QY 3953 TTGCTGCAATTAACAGCCCCCACTCCCGTGCATCCGTTCAAGTCAAGAACCAACGTTT 4012
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QY 4373 CCAGAGTTATCTTGCAACAGCATTAACCTGGTCCCGGTGAACCGCAATCTTCTCAGCCT 4432
Db 3481 CCAGAGTTATCTTGCAACAGCATTAACCTGGTCCCGGTGAACCGCAATCTTCTCAGCCT 3540
QY 4433 TAGTCCCCGAGTACAAGAGAAGCAACCCGCGGTCAAAAAATTCTGAAACCACTCA 4492
Db 3541 TAGTCCCCGAGTACAAGAGAAGCAACCCGCGGTCAAAAAATTCTGAAACCACTCA 3600
QY 4493 AACACCACTCACTTGTGTATCAGAGGAAAAATTGAAGCTCCCGTTAAGAAATCG 4552
Db 3601 AACACCACTCACTTGTGTATCAGAGGAAAAATTGAAGCTCCCGTTAAGAAATCG 3660
QY 4553 AATGATCGCCCCGATTTGGCATAGCCGGTGCATTAAGAACTACAACCTGCTTTCGGGT 4612
Db 3661 AATGATCGCCCCGATTTGGCATAGCCGGTGCATTAAGAACTACAACCTGCTTTCGGGT 3720
QY 4613 TTCCGCGCGAGGCAAGGTACGACCTGGTTCATCAACATTGGAATTAATACAGAAACC 4672
Db 3721 TTCCGCGCGAGGCAAGGTACGACCTGGTTCATCAACATTGGAATTAATACAGAAACC 3780
QY 4673 ACCACTTTACAGAGTGCGAAGAACCATGCGGCACTTAAAAACCTTTGCGGTTCGGCCC 4732
Db 3781 ACCACTTTACAGAGTGCGAAGAACCATGCGGCACTTAAAAACCTTTGCGGTTCGGCCC 3840
QY 4733 TGAATTGTTTAACTCAGAGGCAACCTCGTGTGAAGTCTATGGCTACGCCGACCGCA 4792
Db 3841 TGAATTGTTTAACTCAGAGGCAACCTCGTGTGAAGTCTATGGCTACGCCGACCGCA 3900
QY 4793 ACAGTGAGGACGTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAAGGTGTCTGACGAGAC 4852
Db 3901 ACAGTGAGGACGTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAAGGTGTCTGACGAGAC 3960
QY 4853 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAACTAGACAAACAGCC 4912
Db 3961 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAACTAGACAAACAGCC 4020
QY 4913 GTACACGGCAATTCACCCCGCACCATCTGAATGCGTATTCGTCGCTGTATGAGGGTA 4972
Db 4021 GTACACGGCAATTCACCCCGCACCATCTGAATGCGTATTCGTCGCTGTATGAGGGTA 4080

QY 4973 CAAGAGATGAGTTGGAGCCGCGCGCTCATACCGCACCAAAAAAGGAGAAATATTGCTGACT 5032
Db 4081 CAAGAGATGAGTTGGAGCCGCGCGCTCATACCGCACCAAAAAAGGAGAAATATTGCTGACT 4140
QY 5033 GTCAAGAGAACAGTTGTCAACGACGCAATCCGCTGGGTAGACGAGCGAAGAGTCT 5092
Db 4141 GTCAAGAGAACAGTTGTCAACGACGCAATCCGCTGGGTAGACGAGCGAAGAGTCT 4200
QY 5093 GCCGTCCATCTATAAACGTTGGCCGACCAAGTTTACCAGATTACGCCACGAGACAGGCA 5152
Db 4201 GCCGTCCATCTATAAACGTTGGCCGACCAAGTTTACCAGATTACGCCACGAGACAGGCA 4260
QY 5153 CCGCAAGATGACTGTGTGCTAGGAAAGAAAGTATCCACGCGGTGCGCTGATTTCC 5212
Db 4261 CCGCAAGATGACTGTGTGCTAGGAAAGAAAGTATCCACGCGGTGCGCTGATTTCC 4320
QY 5213 GGAAGCACCCAGAGCAGAAAGCCTTGAAATTGCTACAAAAAGCCTTACATGACGTGGCAG 5272
Db 4321 GGAAGCACCCAGAGCAGAAAGCCTTGAAATTGCTACAAAAAGCCTTACATGACGTGGCAG 4380
QY 5273 ACTTAGTAATGAACATACATCAAGTCTGTCCCATTTCCACTGTAATCTACAGGCATTT 5332
Db 4381 ACTTAGTAATGAACATACATCAAGTCTGTCCCATTTCCACTGTAATCTACAGGCATTT 4440
QY 5333 ACGGAGCCGGAAGAACCCGCTTGAAGTATCACTTAAGTCTTGACAAACCGCGCTAGACA 5392
Db 4441 ACGGAGCCGGAAGAACCCGCTTGAAGTATCACTTAAGTCTTGACAAACCGCGCTAGACA 4500
QY 5393 GAACTGACGCGGACGTAAACCATCTATTGCTGGAATAAGAGTGAAAGAAAGAAATCGACG 5452
Db 4501 GAACTGACGCGGACGTAAACCATCTATTGCTGGAATAAGAGTGAAAGAAAGAAATCGACG 4560
QY 5453 CGGCACTCCAATTAAAGAGTCTGTAAACAGAGCTGAAGATGAAGATGAAGATCGACG 5512
Db 4561 CGGCACTCCAATTAAAGAGTCTGTAAACAGAGCTGAAGATGAAGATGAAGATCGACG 4620
QY 5513 ATGAGTTAGTATGATTTCATCCAGACAGTTGCTTGAAGGAAAGAGATTCAGTACTA 5572
Db 4621 ATGAGTTAGTATGATTTCATCCAGACAGTTGCTTGAAGGAAAGAGATTCAGTACTA 4680
QY 5573 CAAAAGAAAAATTGATTTCGTAATTGCAAGGCAACCAATTCCATCAAGCAACCAAGACA 5632
Db 4681 CAAAAGAAAAATTGATTTCGTAATTGCAAGGCAACCAATTCCATCAAGCAACCAAGACA 4740
QY 5633 TGGCGGAGATAAGGTCCTGTTCCCTAATGACAGGAAAGTAATGAACAATGTGTGCT 5692
Db 4741 TGGCGGAGATAAGGTCCTGTTCCCTAATGACAGGAAAGTAATGAACAATGTGTGCT 4800
QY 5693 ACATATTGGGTGAGACCATGGAAGCAATCCGGAAGTGCCCGGTGACCATTAACCCGT 5752
Db 4801 ACATATTGGGTGAGACCATGGAAGCAATCCGGAAGTGCCCGGTGACCATTAACCCGT 4860
QY 5753 CGTCTAGCCGCCCAAAACGTTGCCGTGCTTGCATGTATGCCATGACGCCAGAAAGGG 5812
Db 4861 CGTCTAGCCGCCCAAAACGTTGCCGTGCTTGCATGTATGCCATGACGCCAGAAAGGG 4920
QY 5813 TCCACAGACTTGAAGCAATTAACGTCAAGAAAGTTACAGTATGCTCTCCACCCCTTC 5872
Db 4921 TCCACAGACTTGAAGCAATTAACGTCAAGAAAGTTACAGTATGCTCTCCACCCCTTC 4980
QY 5873 CTAAGCAAAAAATTAAAGATGTTACAGAAAGTTACGTACAGAAAGTATGCTCTGTTAATC 5932
Db 4981 CTAAGCAAAAAATTAAAGATGTTACAGAAAGTTACGTACAGAAAGTATGCTCTGTTAATC 5040
QY 5933 CGCACACTCCCGCATTCGTTCCCGCCGTAAGTACATAGAAGTGCCAGAACGCTTACCG 5992
Db 5041 CGCACACTCCCGCATTCGTTCCCGCCGTAAGTACATAGAAGTGCCAGAACGCTTACCG 5100
QY 5993 CTCCTCTGACAGAGCCGAGAGGCCCCCGAAGTTGTAGCGACACCGTCAACCATCTACAG 6052
Db 5101 CTCCTCTGACAGAGCCGAGAGGCCCCCGAAGTTGTAGCGACACCGTCAACCATCTACAG 5160

QY	6053	CTGATAACACCTCGCTTGATGTCA	CAGACATCTCACTGATATG	GATGACAGTAGCGAAG	61112
Db	5161	CTGATTAACACCTCGCTTGATGTCA	CAGACATCTCACTGATATG	GATGACAGTAGCGAAG	5220
QY	6113	GCTCACTTTTTTCGAGCTTTTACG	CGGATCGGACCAACTCTATTA	CTAGTATGACAGTTGGT	61722
Db	5221	GCTCACTTTTTTCGAGCTTTTACG	CGGATCGGACCAACTCTATTA	CTAGTATGACAGTTGGT	5280
QY	6173	CGTCAGGACCTAGTTCACTAGAGA	TAGTAGACCGAAGCAGGTGGT	GTGCTGACGTTC	6232
Db	5281	CGTCAGGACCTAGTTCACTAGAGA	TAGTAGACCGAAGCAGGTGGT	GTGCTGACGTTC	5340
QY	6233	ATGCCGTCCAAGAGCCTGCCCTAT	TCCACCGCCCAAGGCTAAAGA	AGATGCGCCGCTGG	6292
Db	5341	ATGCCGTCCAAGAGCCTGCCCTAT	TCCACCGCCCAAGGCTAAAGA	AGATGCGCCGCTGG	5400
QY	6293	CAGCGGCAAGAAAAGAGCCCACT	CCACCGGCAAGCAATAGCTCT	GAGTCCCTCCACTCT	6352
Db	5401	CAGCGGCAAGAAAAGAGCCCACT	CCACCGGCAAGCAATAGCTCT	GAGTCCCTCCACTCT	5460
QY	6353	CTTTTGGTGGGTATCCATGTCCCT	CGGATCAATTTTTCGACGGAGA	GACGGCCGCGCAGG	6412
Db	5461	CTTTTGGTGGGTATCCATGTCCCT	CGGATCAATTTTTCGACGGAGA	GACGGCCGCGCAGG	5520
QY	6413	CAGCGGTACAACCCCTGGCAACA	GAGCCCCACCGATGTGCTATGT	CTTTCCGATCGTTT	6472
Db	5521	CAGCGGTACAACCCCTGGCAACA	GAGCCCCACCGATGTGCTATGT	CTTTCCGATCGTTT	5580
QY	6473	CCGACGGAGAGATTGATGAGCTGA	CGCCGACAGTAAGTCCGAACCC	CGTCCGTGTTG	6532
Db	5581	CCGACGGAGAGATTGATGAGCTGA	CGCCGACAGTAAGTCCGAACCC	CGTCCGTGTTG	5640
QY	6533	GATCATTTTGAACCGGGCGCAAGT	GACTCAATTATTCGTCCCGATC	AGCCGATCTTTTC	6592
Db	5641	GATCATTTTGAACCGGGCGCAAGT	GACTCAATTATTCGTCCCGATC	AGCCGATCTTTTC	5700
QY	6593	CACCTACGCAAGCAGAGACCTTGA	CGCAGAGCAGGAGACTGAATACT	GACTAACCCGGG	6652
Db	5701	CACCTACGCAAGCAGAGACCTTGA	CGCAGAGCAGGAGACTGAATACT	GACTAACCCGGG	5760
QY	6653	TAGTGGGTACATATTTTTCACGGA	CACAGGCCCTGGGCACTTGCAAA	AGAGTCGTTTC	6712
Db	5761	TAGTGGGTACATATTTTTCACGGA	CACAGGCCCTGGGCACTTGCAAA	AGAGTCGTTTC	5820
QY	6713	TGCAGAACCAGCTTACAGAACCGA	CCCTTGAGCGCAATGTCTGAAA	AGATTTCATGCC	6772
Db	5821	TGCAGAACCAGCTTACAGAACCGA	CCCTTGAGCGCAATGTCTGAAA	AGATTTCATGCC	5880
QY	6773	CGGTGCTCGACACGTGGAAGAGA	CAACTCAAACTCAGTTACCATGA	TGCCCCA	6832
Db	5881	CGGTGCTCGACACGTGGAAGAGA	CAACTCAAACTCAGTTACCATGA	TGCCCCA	5940
QY	6833	AAAGCCAACAAAAGTAGGTACCA	GTCTCGTAAAGTAGAATAACAA	AGCCATTAACCACTG	6892
Db	5941	AAAGCCAACAAAAGTAGGTACCA	GTCTCGTAAAGTAGAATAACAA	AGCCATTAACCACTG	6000
QY	6893	AGCGACTACTGTCAAGACTTACGA	CTGTATTAAGTCTTGCCACAGAT	CAGCCAGAAATGCTATA	6952
Db	6001	AGCGACTACTGTCAAGACTTACGA	CTGTATTAAGTCTTGCCACAGAT	CAGCCAGAAATGCTATA	6060
QY	6953	AGATCACTATCCGAAACCAATTGT	ACTCCAGTAGCGTACCGGCGAA	ACTACTCCGATCCAC	7012
Db	6061	AGATCACTATCCGAAACCAATTGT	ACTCCAGTAGCGTACCGGCGAA	ACTACTCCGATCCAC	6120
QY	7013	AGTTGCTGTAGCTGTCTGTAA	CAACTATCTGCATGAGAACTAT	CCGACAGTAGACTCTT	7072
Db	6121	AGTTGCTGTAGCTGTCTGTAA	CAACTATCTGCATGAGAACTAT	CCGACAGTAGACTCTT	6180
QY	7073	ATCAGATTACTGACGAGTAGATG	CTTACTTTGGATATGTTAGACG	AGACAGTCCGATGCC	7132
Db	6181	ATCAGATTACTGACGAGTAGATG	CTTACTTTGGATATGTTAGACG	AGACAGTCCGATGCC	6240
QY	7133	TGGATACTGCAACCTTCTGCCCC	CGTTAAGCTTAGAAGTTACCCG	AAAAAATGATGATATA	7192

Db	6241	TGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATA	6300
QY	7193	GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCCGATGCAGAACACGGCTACAAAATGTGC	7252
Db	6301	GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCCGATGCAGAACACGGCTACAAAATGTGC	6360
QY	7253	TCATTGCCGCAACTAAAAAGAAATTGCAACGTCACCGAGATGCCGTGAACCTGCCAACCTGG	7312
Db	6361	TCATTGCCGCAACTAAAAAGAAATTGCAACGTCACCGAGATGCCGTGAACCTGCCAACCTGG	6420
QY	7313	ACTCAGCGACATTCATGTCTCGAATGCTTCGAAAAATATGCATGTAAATGACGAGTATTGGG	7372
Db	6421	ACTCAGCGACATTCATGTCTCGAATGCTTCGAAAAATATGCATGTAAATGACGAGTATTGGG	6480
QY	7373	AGGAGTTCGCTCGGAAAGCCAAATTAGATTACCACTGAGTTTGTCAACCGCATATGTAGCTA	7432
Db	6481	AGGAGTTCGCTCGGAAAGCCAAATTAGATTACCACTGAGTTTGTCAACCGCATATGTAGCTA	6540
QY	7433	GACTGAAAGGCCCTAAGGCCGCCGCACTATTTCGAAAGACGTATATTGGTCCCATTTGC	7492
Db	6541	GACTGAAAGGCCCTAAGGCCGCCGCACTATTTCGAAAGACGTATATTGGTCCCATTTGC	6600
QY	7493	AAGAAGTGCCTATGAGTATGATTTCGTCAATGACATGAAAAAGAGACGTGAAGTTTACACCA	7552
Db	6601	AAGAAGTGCCTATGAGTATGATTTCGTCAATGACATGAAAAAGAGACGTGAAGTTTACACCA	6660
QY	7553	GCACGAAACACACAGAAAGAAAGACCCGAAAGTACAAAGTATACAAAGCCGACAAACCCCTGG	7612
Db	6661	GCACGAAACACACAGAAAGAAAGACCCGAAAGTACAAAGTATACAAAGCCGACAAACCCCTGG	6720
QY	7613	CGACTGCTTACTTATGCGGGATTCAACGGGAATTAGTCGTAGGCTTACCGCCGTCTTGC	7672
Db	6721	CGACTGCTTACTTATGCGGGATTCAACGGGAATTAGTCGTAGGCTTACCGCCGTCTTGC	6780
QY	7673	TTCCAAACATTCACACGCTTTTTCACATGTCGGCGAGAGATTTTGTATGCAATCATAGCAG	7732
Db	6781	TTCCAAACATTCACACGCTTTTTCACATGTCGGCGAGAGATTTTGTATGCAATCATAGCAG	6840
QY	7733	AACACTTCAAGCAAGGCGACCCCGTACTGAGACGGATATCGCATCATTCGACAAAAGCC	7792
Db	6841	AACACTTCAAGCAAGGCGACCCCGTACTGAGACGGATATCGCATCATTCGACAAAAGCC	6900
QY	7793	AAGACGACGCTATGGCGTTAACCCGTCGTGATCTTTGAGAGACCTGGGTGTGATCAAC	7852
Db	6901	AAGACGACGCTATGGCGTTAACCCGTCGTGATCTTTGAGAGACCTGGGTGTGATCAAC	6960
QY	7853	CACACTCGACTTGTATCGAGTGCGCCCTTGGAGAAATATCATCCACCCATCTACCTACGG	7912
Db	6961	CACACTCGACTTGTATCGAGTGCGCCCTTGGAGAAATATCATCCACCCATCTACCTACGG	7020
QY	7913	GTACTCGTTTAAATTCGGGGCGATGATGAATCCGGAATGTTCTCTACACTTTTGTCA	7972
Db	7021	GTACTCGTTTAAATTCGGGGCGATGATGAATCCGGAATGTTCTCTACACTTTTGTCA	7080
QY	7973	ACACAGTTTGAATGTGCTTATCGCAGCAGAGTACTAGAAGAGCGGCTTAAAAAGTCCA	8032
Db	7081	ACACAGTTTGAATGTGCTTATCGCAGCAGAGTACTAGAAGAGCGGCTTAAAAAGTCCA	7140
QY	8033	GATGTGACGCGTTCAATTGGCGACGACAAACATCATACATGAGTAGTATCTGACAAAGAAA	8092
Db	7141	GATGTGACGCGTTCAATTGGCGACGACAAACATCATACATGAGTAGTATCTGACAAAGAAA	7200
QY	8093	TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAAGTTAAGATCATCGACGCACTCATCG	8152
Db	7201	TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAAGTTAAGATCATCGACGCACTCATCG	7260
QY	8153	GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTGGTTACTTCCACAG	8212
Db	7261	GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTGGTTACTTCCACAG	7320
QY	8213	CGTGCCGCGTGCGGATCCCTGAAAAAGCTGTTTAAGTTGGTAAACCGCTCCACGCCG	8272

Db	7321	CGTGCCCGCTGGCGGATCCCTCGAAAAAGGCTGTTTAAGTTGGGTAAACCGCTCCACCGG	7380
Qy	8273	ACGACGACGAAGACGAAGAAGACGCGCTCTGTAGATGAAACAAAGCGGTGTTTA	8332
Db	7381	ACGACGACGAAGACGAAGAAGACGCGCTCTGTAGATGAAACAAAGCGGTGTTTA	7440
Qy	8333	GAGTAGGTATAACAGGCACCTTACAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA	8392
Db	7441	GAGTAGGTATAACAGGCACCTTACAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA	7500
Qy	8393	TTACACCTGTCTACTGGCATTTGAGAACTTTGGCCAGACAAAGACATTCCAGCCA	8452
Db	7501	TTACACCTGTCTACTGGCATTTGAGAACTTTGGCCAGACAAAGACATTCCAGCCA	7560
Qy	8453	TCAGAGGGGAATTAAGCATCTCTACGGTGTCTTAATAGTCAGCATAGTACATTTCAT	8512
Db	7561	TCAGAGGGGAATTAAGCATCTCTACGGTGTCTTAATAGTCAGCATAGTACATTTCAT	7620
Qy	8513	CTGACTAATACTACAACACCAACCACTT	8539
Db	7621	CTGACTAATACTACAACACCAACCACTT	7647
RESULT 9			
AAA90386	ID AAA90386 standard; DNA; 9951 BP.		
XX	AC	AAA90386;	
XX	DT	10-JAN-2001 (first entry)	
XX	DE	Sindbis expression vector pSindRep5 DNA sequence.	
KW	KW	Nucleic acid identification; exogenous protein; drug screening;	
KW	KW	recombinant expression; pSindRep5; mammalian expression system; cyclic;	
KW	KW	circular; ds.	
XX	OS	Synthetic.	
OS	OS	Sindbis virus.	
XX	PN	JP2000189173-A.	
XX	PD	11-JUL-2000.	
XX	PF	23-AUG-1999; 99JP-00236220.	
XX	PR	17-NOV-1998; 98US-00193707.	
PR	PR	17-NOV-1998; 98WO-US024520.	
XX	PA	(CYTO-) CYTOS BIOTECHNOLOGY GMBH.	
XX	DR	WPI; 2000-551637/51.	
XX	PT	Identifying a recombinant nucleic acid to identify and isolate various	
PT	PT	cellular proteins, comprises culturing a composition comprising	
PT	PT	eukaryotic host cells and identifying a cell comprising recombinant	
PT	PT	nucleic acid.	
XX	PS	Example 7; Fig 11A-C; 56pp; Japanese.	
XX	CC	The invention relates to the identification of a recombinant nucleic acid	
CC	CC	encoding an exogenous protein having a selected property. The method	
CC	CC	comprises preparing populations of eukaryotic host cells, where each cell	
CC	CC	comprises an expression vector encoding a different exogenous protein.	
CC	CC	The host cells are cultured under suitable conditions and the nucleic	
CC	CC	acid which encodes the exogenous protein is identified. The method is	
CC	CC	useful for the identification and isolation of proteins with a selected	
CC	CC	property. Typical applications of the nucleic acid and the exogenous	
CC	CC	protein are in isolation of new growth factors, cytokines, membrane	
CC	CC	receptors, cytoplasmic, organelle or nuclear proteins, all of which may	
CC	CC	be useful as therapeutic agents or therapeutic targets, e.g., pro-	
CC	CC	apoptotic or tumour suppressing proteins, regulators of cell	
CC	CC	proliferation or of metabolic processes. The protein can also be used to	

CC screen for ligands and specific modulators of activity. The method of the
CC invention allows the direct cloning of full length cDNAs in one step. It
CC facilitates direct expression of the protein without the need to perform
CC further procedures such as subcloning and establishment of a cell line
CC for protein production. The method allows a protein of interest (rather
CC than a partial DNA sequence) to be isolated and, since a wide range of
CC cell types can be used, they can be expressed in a correctly folded and
CC glycosylated form. The present sequence represents the Sindbis expression
CC vector psinRep5 which was used in the exemplifications of the invention.
CC This patent is related to WO9325876

Query Match	89.4%;	Score 7637.4;	DB 3;	Length 9951;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 7641; Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;

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Oy      893  ATTGACGGCGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCCTACCATCACAA  952
          |||||||
Db      1  ATTGACGGCGTAGTACACACTATTGAATCAAAACAGCCGACCAATTGCCTACCATCACAA  60

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QY      953 TGGAGAAGCCAGTAGTAAACGTAGACCGTAGACCCCCCAGATCCGTTTGTCGTCAACTGC   1012
        |||||
Db       61 TGGAGAAGCCAGTAGTAAACGTAGACCGTAGACCCCCCAGATCCGTTTGTCGTCAACTGC   120
```

Oy	1013	AAAAAGCTTCCCGCAATTGAGGTAGTACACAGCAGCTCACTCCAAATGACCATGCTA	1072
Db	121	AAAAAGCTTCCCGCAATTGAGGTAGTACACAGCAGCTCACTCCAAATGACCATGCTA	180

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QY      1073 ATGCCAGACATTTTCGACTCTGGCCAGTAAACTAATCGAGCTTGAGGTTCTTACCACAG   1132
          |||||
DB      181  ATGCCAGACATTTTCGACTCTGGCCAGTAAACTAATCGAGCTTGAGGTTCTTACCACAG   240

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OY      1133 CGACGATCTTGACATAGGCAGCGCACCCGGCTCGTAGATGTTTTCCGAGCACCAGTATC 1192
        |||||
DB      241  CGACGATCTTGACATAGGCAGCGCACCCGGCTCGTAGATGTTTTCCGAGCACCAGTATC 300
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QY      1193 ATTGTGTCGCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAATAACGCCAGTA   1252
        |||||
DB      301 ATTGTGTCGCCCATGCGTAGTCCAGAAGACCCGGACCGCATGATGAATAACGCCAGTA   360
```

Oy 1253 AACTGGCGAAAAAGCCGTCGAAGATTACAAACAAGAATTGCATGAGAAGATTAAAGATC 1312

Db 361 AACTGGCGAAAAAGCCGTCGAAGATTACAAACAAGAATTGCATGAGAAGATTAAAGATC 420

[illegible][illegible][illegible]

Oy		1493	CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTAACCCTGCGTACAACACCAACTGGG	1552
Db		601	CCACCCAGTTCATGTTCTCGGCTATGGCAGGTTCGTAACCCTGCGTACAACACCAACTGGG	660

[illegible]

Oy	1613 GTAGGACAGAAAATTGTGCATAATGAGGAAGAAGCATTGAAGCCCGGGTCGCCGGCTTT	1672
Dδ	721 GTAGGACAGAAATTGTGCATAATGAGGAAGAAGCATTGAAGCCCGGGTCGCCGGCTTT	780

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Ox      1673 ATTTCTCCGTAGGATCGACACTTATTCCAGAACAACAGAGCCAGCTTGCAAGCTGGCATC 1732
          |||||
Db      781 ATTTCTCCGTAGGATCGACACTTATCCAGAACACAGAGCCAGCTTGCAAGCTGGCATC 840
```

QY 1733 TTCATCGGTGTTCCACTTGAATGAAAGCAGTCGTACACTTCCGCTGTGATACAGTGG 1792
| | | | |
Db 841 TTCCATCGGTGTTCCACTTGAATGAAAGCAGTCGTACACTTCCGCTGTGATACAGTGG 900
| | | | |
QY 1793 TGAGTTGGCAAGGCTACGTAAGTGAAGAAATCACCATCAGTCCCGGATCAGGGAGAA 1852
| | | | |
Db 901 TGAGTTGGCAAGGCTACGTAAGTGAAGAAATCACCATCAGTCCCGGATCAGGGAGAA 960
| | | | |
QY 1853 CCGTGGATACGGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAAGTTACTGACA 1912
| | | | |
Db 961 CCGTGGATACGGGTTACACACAATAGCGAGGGCTTCTTGCTATGCAAAAGTTACTGACA 1020
| | | | |
QY 1913 CAGTAAAGAGAAACGGGTATCGTTCCTGTGTGACAGTACATCCGGCCACCATATGCG 1972
| | | | |
Db 1021 CAGTAAAGAGAAACGGGTATCGTTCCTGTGTGACAGTACATCCGGCCACCATATGCG 1080
| | | | |
QY 1973 ATCAGATGACTGTATTAATGCGCACGGATATATCACCTGACGATGCACAAAAAGTTCTGG 2032
| | | | |
Db 1081 ATCAGATGACTGTATTAATGCGCACGGATATATCACCTGACGATGCACAAAAAGTTCTGG 1140
| | | | |
QY 2033 TTGGGCTCAACCGGAATTGTATTAAACGGTAGAGCTAACAGAAACCAACACCATGCG 2092
| | | | |
Db 1141 TTGGGCTCAACCGGAATTGTATTAAACGGTAGAGCTAACAGAAACCAACACCATGCG 1200
| | | | |
QY 2093 AAAATTACCTTCTGCCGATCATAGCACAGGGTTCAGCAATGGGCTAAGAGCGCAAGG 2152
| | | | |
Db 1201 AAAATTACCTTCTGCCGATCATAGCACAGGGTTCAGCAATGGGCTAAGAGCGCAAGG 1260
| | | | |
QY 2153 ATGATCTTGATTAACGAGAAATGCTGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
| | | | |
Db 1261 ATGATCTTGATTAACGAGAAATGCTGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
| | | | |
QY 2213 TGTGGCGTTTCGCACTAAGAAAGTACATTGTTTATCGCCCACTGGAACGAGACCT 2272
| | | | |
Db 1321 TGTGGCGTTTCGCACTAAGAAAGTACATTGTTTATCGCCCACTGGAACGAGACCT 1380
| | | | |
QY 2273 GCGTAAAGTCCAGCCTCTTTAGCGCTTTTCCCATGTCGTCGTAAGAGACGACCTCTT 2332
| | | | |
Db 1381 GCGTAAAGTCCAGCCTCTTTAGCGCTTTTCCCATGTCGTCGTAAGAGACGACCTCTT 1440
| | | | |
QY 2333 TGCCCATGTCGCTGAGGCGAAGATTGAAACTGGCATTGCAACCAAGAGAGAAAAAC 2392
| | | | |
Db 1441 TGCCCATGTCGCTGAGGCGAAGATTGAAACTGGCATTGCAACCAAGAGAGAAAAAC 1500
| | | | |
QY 2393 TGCTGCAAGTCTCGAGGAATTAGTCATGAGAGCCCAAGGCTGTTTTGAGGATGCTCAGG 2452
| | | | |
Db 1501 TGCTGCAAGTCTCGAGGAATTAGTCATGAGAGCCCAAGGCTGTTTTGAGGATGCTCAGG 1560
| | | | |
QY 2453 AGGAAGCAGAGCGGAGAAAGTCCGAGAGCACTTCCACATTAAGTGGCAGACAAAGGCA 2512
| | | | |
Db 1561 AGGAAGCAGAGCGGAGAAAGTCCGAGAGCACTTCCACATTAAGTGGCAGACAAAGGCA 1620
| | | | |
QY 2513 TCGAGGACCCGAGAAAGTGTCTGCGAAGTGGAGGGGCTCCAGCGGACATCGAGCAG 2572
| | | | |
Db 1621 TCGAGGACCCGAGAGAAAGTGTCTGCGAAGTGGAGGGGCTCCAGCGGACATCGAGCAG 1680
| | | | |
QY 2573 CATTAAGTGAACCCCGCGGTACGTAAGGATATATACCTCAAGCAATGACCGTATGA 2632
| | | | |
Db 1681 CATTAAGTGAACCCCGCGGTACGTAAGGATATATACCTCAAGCAATGACCGTATGA 1740
| | | | |
QY 2633 TCGGACAGTATATCGTTGTCTCGCCAAACTGTGCTGAAGAAATGCCAAACTCGCACAG 2692
| | | | |
Db 1741 TCGGACAGTATATCGTTGTCTCGCCAAACTGTGCTGAAGAAATGCCAAACTCGCACAG 1800
| | | | |
QY 2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAGGAAGGTACG 2752
| | | | |
Db 1801 CGCACCCGCTAGCAGATCAGGTTAAGATCATTAACACACTCCGGAAGATCAGGAAGGTACG 1860
| | | | |
QY 2753 CGGTGAAACCATACGACGCTAAAGTACTGATGCCAGAGAGGTGCCGTACCATGCGCAG 2812
| | | | |
Db 1861 CGGTGAAACCATACGACGCTAAAGTACTGATGCCAGAGAGGTGCCGTACCATGCGCAG 1920
| | | | |
QY 2813 AATTCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAACGAAGAGAGTTGTGAACC 2872
| | | | |

Db 1921 AATTCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAAAGAAAGAGAGTTGTGAACC 1980
| | | | |
QY 2873 GCAAACTATATCCACATTGGCATGCAATGCCCCCGCCAAAGAAATACAGAAAGAGAGCAGTACA 2932
| | | | |
Db 1981 GCAAACTATATCCACATTGGCATGCAATGCCCCCGCCAAAGAAATACAGAAAGAGAGCAGTACA 2040
| | | | |
QY 2933 AGGTTACAAAGCAGAGCTTGCAGAAACAGAGTACGTGTTGAAGTGGACAAAGCGTT 2992
| | | | |
Db 2041 AGGTTACAAAGCAGAGCTTGCAGAAACAGAGTACGTGTTGAAGTGGACAAAGCGTT 2100
| | | | |
QY 2993 GCGTTAAGAAAGAAAGCCCTCAGGTCTGCTCTCGGAGAACTGACCAACCTCCCT 3052
| | | | |
Db 2101 GCGTTAAGAAAGAAAGCCCTCAGGTCTGCTCTCGGAGAACTGACCAACCTCCCT 2160
| | | | |
QY 3053 ATCATGAGCTAGCTCTGAGAGGACTGAAGACCCGACCTGCGCTCCCGTACAGGTGCAAA 3112
| | | | |
Db 2161 ATCATGAGCTAGCTCTGAGAGGACTGAAGACCCGACCTGCGCTCCCGTACAGGTGCAAA 2220
| | | | |
QY 3113 CAATAGGAGTATAGGCACACCGGGGTCGGGCAAGTCACTATTATCAAGTCAACTGTCA 3172
| | | | |
Db 2221 CAATAGGAGTATAGGCACACCGGGGTCGGGCAAGTCACTATTATCAAGTCAACTGTCA 2280
| | | | |
QY 3173 CCGCACAGATCTGTATACAGCGGAAAGAAAGAAATGTCGCGAAATTGAGCGCGAG 3232
| | | | |
Db 2281 CCGCACAGATCTGTATACAGCGGAAAGAAAGAAATGTCGCGAAATTGAGCGCGAG 2340
| | | | |
QY 3233 TGCTAAGACTGAGGGGTATGAGATTACGTGGAAGACAGTAGATTCCGTTATGCTCAAG 3292
| | | | |
Db 2341 TGCTAAGACTGAGGGGTATGAGATTACGTGGAAGACAGTAGATTCCGTTATGCTCAAG 2400
| | | | |
QY 3293 GATGCCACAAAGCCGTAGAAAGTCTGTACGTTGACGAAGCGTTCCGCTGCCACGCAAGAG 3352
| | | | |
Db 2401 GATGCCACAAAGCCGTAGAAAGTCTGTACGTTGACGAAGCGTTCCGCTGCCACGCAAGAG 2460
| | | | |
QY 3353 CACTACTTGCTTGAATTGCTATTCGTCAAGCCCCCGCAAGAAAGTACTATGCGGAGACC 3412
| | | | |
Db 2461 CACTACTTGCTTGAATTGCTATTCGTCAAGCCCCCGCAAGAAAGTACTATGCGGAGACC 2520
| | | | |
QY 3413 CCATGCAATGCGGATCTTCAACATGATGCAACTAAAGTACATTCAATCACCCCTGAAA 3472
| | | | |
Db 2521 CCATGCAATGCGGATCTTCAACATGATGCAACTAAAGTACATTCAATCACCCCTGAAA 2580
| | | | |
QY 3473 AAGACATATGACCAAGACATCTCAAGTATATCTCCGCGTTGCACACAGCCAGTTA 3532
| | | | |
Db 2581 AAGACATATGACCAAGACATCTCAAGTATATCTCCGCGTTGCACACAGCCAGTTA 2640
| | | | |
QY 3533 CAGCTATTGTATGACACTGCACTTAAGTGAAGATGAACCAAGAACCCGTGCAAGA 3592
| | | | |
Db 2641 CAGCTATTGTATGACACTGCACTTAAGTGAAGATGAACCAAGAACCCGTGCAAGA 2700
| | | | |
QY 3593 AGAACATTGAATCGATATTAACAGGGGCCACAAAGCCGAAGGGGATATCATCTGTA 3652
| | | | |
Db 2701 AGAACATTGAATCGATATTAACAGGGGCCACAAAGCCGAAGGGGATATCATCTGTA 2760
| | | | |
QY 3653 CATGTTTCGCGGGTGGTTAAGCAATTGCAAAATCGACTATCCCGGACATGAAGTAAATGA 3712
| | | | |
Db 2761 CATGTTTCGCGGGTGGTTAAGCAAAATGCAAAATCGACTATCCCGGACATGAAGTAAATGA 2820
| | | | |
QY 3713 CAGCCGCGGCTCACAAGGGCTAAACAGAAAGAGTGTATGCCGTCGGCAAAAAGTCA 3772
| | | | |
Db 2821 CAGCCGCGGCTCACAAGGGCTAAACAGAAAGAGTGTATGCCGTCGGCAAAAAGTCA 2880
| | | | |
QY 3773 ATGAAAAACCACTGTACGCGATCAATCAGAGCATGTGAAGTGTGCTACCCGCACTG 3832
| | | | |
Db 2881 ATGAAAAACCACTGTACGCGATCAATCAGAGCATGTGAAGTGTGCTACCCGCACTG 2940
| | | | |
QY 3833 AGGACAGGCTAGTGTGAAGAACTTGCAGGGCGACCCCATGGAATTAAAGACCCCACTAACA 3892
| | | | |
Db 2941 AGGACAGGCTAGTGTGAAGAACTTGCAGGGCGACCCCATGGAATTAAAGACCCCACTAACA 3000
| | | | |
QY 3893 TACTTAAAGAACTTTCAGGCTACTATAGAGACTGGAAAGCTGAACACAAAGGGAATAA 3952
| | | | |

Db 3001 TACCTAAAGNAACTTTCAGGCTACTATAGAGACTGGGAAGCTGAACAAGGAATAA 3060
QY 3953 TTGCTGCATAATAACAGCCCCCACTCCCCGTCGCAATCCGTTCAAGTGAAGAACCAAGTTT 4012
Db 3061 TTGCTGCATAATAACAGCCCCCACTCCCCGTCGCAATCCGTTCAAGTGAAGAACCAAGTTT 3120
QY 4013 GCTGGGCGGAAAGCATTTGGAACCGATACTAGCCACGGCCGGTATCGTACTTAAACCGGTGCC 4072
Db 3121 GCTGGGCGGAAAGCATTTGGAACCGATACTAGCCACGGCCGGTATCGTACTTAAACCGGTGCC 3180
QY 4073 AGTGAAGCGAATGTTCCACAGTTTGGCGATGACAAACCAATTCGGCCATTACGCCCT 4132
Db 3181 AGTGAAGCGAATGTTCCACAGTTTGGCGATGACAAACCAATTCGGCCATTACGCCCT 3240
QY 4133 TAGACGTAATTGCAATTAAGTTTTTCGGCATGGAAGCTTGACAAAGCGAAGCTGTTTTCTAAAC 4192
Db 3241 TAGACGTAATTGCAATTAAGTTTTTCGGCATGGAAGCTTGACAAAGCGAAGCTGTTTTCTAAAC 3300
QY 4193 AGAGCATCCCACTAAACGTACCATCCCGCCGATTCAGCGAGCCGGTAGCTCATTTGGGACA 4252
Db 3301 AGAGCATCCCACTAAACGTACCATCCCGCCGATTCAGCGAGCCGGTAGCTCATTTGGGACA 3360
QY 4253 ACAGCCCCAGGAACCCGCAAGTATGGGTACGATCAAGCCATTGGCCGCCAATCTCCCGTA 4312
Db 3361 ACAGCCCCAGGAACCCGCAAGTATGGGTACGATCAAGCCATTGGCCGCCAATCTCCCGTA 3420
QY 4313 GATTTCCGGTGTTCAGCTAGCTGGGAAGGCAACAACCTGATTTGAGACGGGGAGAA 4372
Db 3421 GATTTCCGGTGTTCAGCTAGCTGGGAAGGCAACAACCTGATTTGAGACGGGGAGAA 3480
QY 4373 CCAGAGTTATCTGTGACACAGCATAACTGTCCTGGTGAACCGCAATCTTCTCAGCCT 4432
Db 3481 CCAGAGTTATCTGTGACACAGCATAACTGTCCTGGTGAACCGCAATCTTCTCAGCCT 3540
QY 4433 TAGTCCCCCGAGTACAAAGGAAGCAACCCGCGCCGTCAAAAATTCTTGAACCAAGTTCA 4492
Db 3541 TAGTCCCCCGAGTACAAAGGAAGCAACCCGCGCCGTCAAAAATTCTTGAACCAAGTTCA 3600
QY 4493 AACACCACTCAGTACTTGTGTATCAGAGAAAAAATTGAAGCTCCCCGTAAGAGAAATCG 4552
Db 3601 AACACCACTCAGTACTTGTGTATCAGAGAAAAAATTGAAGCTCCCCGTAAGAGAAATCG 3660
QY 4553 AATGATCGCCCCGATTTGGCATAGCCGGTGAAGATTAAGAACTACAACTGGCTTTGGGT 4612
Db 3661 AATGATCGCCCCGATTTGGCATAGCCGGTGAAGATTAAGAACTACAACTGGCTTTGGGT 3720
QY 4613 TTCCGCGCGAGCAAGCAAGTACGACCTGGTTCATCAACATTGGAATAATAACAGAAACC 4672
Db 3721 TTCCGCGCGAGCAAGCAAGTACGACCTGGTTCATCAACATTGGAATAATAACAGAAACC 3780
QY 4673 ACCACTTTACGACGTGCGAAGACCATGCGCGCACTTAAAAACCTTTGCGGTTGGCCC 4732
Db 3781 ACCACTTTACGACGTGCGAAGACCATGCGCGCACTTAAAAACCTTTGCGGTTGGCCC 3840
QY 4733 TGAATTGTTTAACTCAGAGGCAACCTCGTGTGAAGTCTATGCTACGCCGACCGCA 4792
Db 3841 TGAATTGCTTAACTCAGAGGCAACCTCGTGTGAAGTCTATGCTACGCCGACCGCA 3900
QY 4793 ACAGTGAGGACGTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAAGGTGTGACGCGAGAC 4852
Db 3901 ACAGTGAGGACGTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAAGGTGTGACGCGAGAC 3960
QY 4853 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAACTAGACAACAGCC 4912
Db 3961 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAACTAGACAACAGCC 4020
QY 4913 GTACACGGCAATTCAACCCCGCACCATCTGAATTGCGTGATTTCCGTTATGAGGGTA 4972
Db 4021 GTACACGGCAATTCAACCCCGCACCATCTGAATTGCGTGATTTCCGTTATGAGGGTA 4080
QY 4973 CAAGAGATGAGTTGAGCGCGCGCTCATACCGCAACAAAAAGGAGAGATATTGCTGACT 5032
Db 4081 CAAGAGATGAGTTGAGCGCGCGCTCATACCGCAACAAAAAGGAGATATTGCTGACT 4140

QY 5033 GTCAAGAGGAGCAGTGTGTCAACCGCAGCCAAATCCGCTGGGTAGACGAGCGAAGGAGTCT 5092
Db 4141 GTCAAGAGGAGCAGTGTGTCAACCGCAGCCAAATCCGCTGGGTAGACGAGCGAAGGAGTCT 4200
QY 5093 GCCGTGCCATCTATAACGTTGGCCGACCAAGTTTACCGATTACGCCACGGAGACAGGCA 5152
Db 4201 GCCGTGCCATCTATAACGTTGGCCGACCAAGTTTACCGATTACGCCACGGAGACAGGCA 4260
QY 5153 CCGAAGATGACTGTGTGCTAGGAAAGAAAGTGATCCACGGCGTCCGCCCTGATTTCC 5212
Db 4261 CCGAAGATGACTGTGTGCTAGGAAAGAAAGTGATCCACGGCGTCCGCCCTGATTTCC 4320
QY 5213 GGAAGCACCAGAAAGCAGAAAGCCTTGAAATTGCTACAAAAAGCCTTACCATGCAAGTGGCAG 5272
Db 4321 GGAAGCACCAGAAAGCAGAAAGCCTTGAAATTGCTACAAAAAGCCTTACCATGCAAGTGGCAG 4380
QY 5273 ACTTAGTAAATGAACATTAACATCAAGTCTGTCCCATTTCCACTGCTATCTACAGGCAATT 5332
Db 4381 ACTTAGTAAATGAACATTAACATCAAGTCTGTCCCATTTCCACTGCTATCTACAGGCAATT 4440
QY 5333 ACGCAGCCGGAAGAAAGCAGCCTTGAAAGTACCTTAAGTGTGAACCGCGCTAGACA 5392
Db 4441 ACGCAGCCGGAAGAAAGCAGCCTTGAAAGTACCTTAAGTGTGAACCGCGCTAGACA 4500
QY 5393 GAAGTGAAGCGGACGTAAACCATCTATGCTGATTAAGAGTGAAGAAAGAAATCGACG 5452
Db 4501 GAAGTGAAGCGGACGTAAACCATCTATGCTGATTAAGAGTGAAGAAAGAAATCGACG 4560
QY 5453 CGGCACTCCAACTTAAGAGTCTGTAAACAGAGCTGAAGAGTGAAGATATGAGATCGACG 5512
Db 4561 CGGCACTCCAACTTAAGAGTCTGTAAACAGAGCTGAAGAGTGAAGATATGAGATCGACG 4620
QY 5513 ATGAGTTAGTATGGAATTCAATCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTA 5572
Db 4621 ATGAGTTAGTATGGAATTCAATCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTA 4680
QY 5573 CAAAAAGAAAAATTGTAATTCGTAATTCGAAGGCAACCAATTCATCAAGCAACAAAAAGACA 5632
Db 4681 CAAAAAGAAAAATTGTAATTCGTAATTCGAAGGCAACCAATTCATCAAGCAACAAAAAGACA 4740
QY 5633 TGGCGGAGTAAAGTCTCTGTTCCCTAATGACCAAGAAAGTAATGAACAATGTGTGCCT 5692
Db 4741 TGGCGGAGTAAAGTCTCTGTTCCCTAATGACCAAGAAAGTAATGAACAATGTGTGCCT 4800
QY 5693 ACATATTGGGTGAGACCATGGAAGCAATCCGCAAAAAGTGCCCGGTGACCAATAACCCGT 5752
Db 4801 ACATATTGGGTGAGACCATGGAAGCAATCCGCAAAAAGTGCCCGGTGACCAATAACCCGT 4860
QY 5753 CGTCTAGCCCGCCAAAAAGTTCGCGCTTGCATGTATGCAAGCCAGAAAAAGGG 5812
Db 4861 CGTCTAGCCCGCCAAAAAGTTCGCGCTTGCATGTATGCAAGCCAGAAAAAGGG 4920
QY 5813 TCCACAGACTTAGAAGCAATAACGTCAAGAAAGTTACAGTATGCTCCCAACCCCTTC 5872
Db 4921 TCCACAGACTTAGAAGCAATAACGTCAAGAAAGTTACAGTATGCTCCCAACCCCTTC 4980
QY 5873 CTAAGCAAAAAATTAAAGATGTTCAAGAGTTCAAGTGCACGAAAGTAGTCTGTTTAATC 5932
Db 4981 CTAAGCAAAAAATTAAAGATGTTCAAGAGTTCAAGTGCACGAAAGTAGTCTGTTTAATC 5040
QY 5933 CGCAGACTCCCGCATTTGTTCCCGCCGTTAAGTACATAGAAGTGCCAGAAACAGCCTACCG 5992
Db 5041 CGCAGACTCCCGCATTTGTTCCCGCCGTTAAGTACATAGAAGTGCCAGAAACAGCCTACCG 5100
QY 5993 CTCCTCTGCAAGGCGGAGGAGGCGCCGAAAGTTGTAGCGACACCGTCAACCATCTACAG 6052
Db 5101 CTCCTCTGCAAGGCGGAGGAGGCGCCGAAAGTTGTAGCGACACCGTCAACCATCTACAG 5160
QY 6053 CTGATAACAACCTCGCTTGATGTCAAGACATCTCACTGGATATGATGACAGTAGCGAAG 6112
Db 5161 CTGATAACAACCTCGCTTGATGTCAAGACATCTCACTGGATATGATGACAGTAGCGAAG 5220

QY	6113	GCTCACTTTTTCGAGCTTTAGCGGATCGGACCACTCTATTACTAGTATGACAGTTGGT	61172
Db	5221	GCTCACTTTTTCGAGCTTTAGCGGATCGGACCACTCTATTACTAGTATGACAGTTGGT	5280
QY	6173	CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGGAAGCAGGTGTGTGCTGACGTTT	6232
Db	5281	CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGGAAGCAGGTGTGTGCTGACGTTT	5340
QY	6233	ATGCCGTCCAGAGAGCCTGCCCTATTCCACCGCCCAAGGCTAAAGAAGATGACCCGCTGG	6292
Db	5341	ATGCCGTCCAGAGAGCCTGCCCTATTCCACCGCCCAAGGCTAAAGAAGATGACCCGCTGG	5400
QY	6293	CAGCGGCAAGAAAAGAGGCCCACTCCACCGGCAAGCAATAGCTTGAAGTCCCTCCACTCT	6352
Db	5401	CAGCGGCAAGAAAAGAGGCCCACTCCACCGGCAAGCAATAGCTTGAAGTCCCTCCACTCT	5460
QY	6353	CTTTTGGTGGGATATCCATGTCTCCCTCGGATCAATTTTTCGACGAGAGACGGCCCGCAGG	6412
Db	5461	CTTTTGGTGGGATATCCATGTCTCCCTCGGATCAATTTTTCGACGAGAGACGGCCCGCAGG	5520
QY	6413	CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCTATGTCTTTCGATCGTTT	6472
Db	5521	CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCTATGTCTTTCGATCGTTT	5580
QY	6473	CCGACGGAGAGATTGATGAGCTGAGCCCGCAGAGTAACTGAGTCCGAACCCGTCGTGTTG	6532
Db	5581	CCGACGGAGAGATTGATGAGCTGAGCCCGCAGAGTAACTGAGTCCGAACCCGTCGTGTTG	5640
QY	6533	GATCATTTTGAACCGGGCGAAGTGAATCTCAATTATATCGTCCCGATCAGCCGATCTTTT	6592
Db	5641	GATCATTTTGAACCGGGCGAAGTGAATCTCAATTATATCGTCCCGATCAGCCGATCTTTT	5700
QY	6593	CACTACGCAAGCAGAGACGTTAGACCGCAGGACGAGGAGACTGAATCTGACTAACCGGGG	6652
Db	5701	CACTACGCAAGCAGAGACGTTAGACCGCAGGACGAGGAGACTGAATCTGACTAACCGGGG	5760
QY	6653	TAGGTGGGTACATATTTTTCGACGGACACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTT	6712
Db	5761	TAGGTGGGTACATATTTTTCGACGGACACACAGGCCCTGGGCACTTGCAAAAGAAGTCCGTT	5820
QY	6713	TGCAGAACCAAGCTTACAGAACCGACTTGGAGCGCAATGTCTTGAAAGAATTCATGCCC	6772
Db	5821	TGCAGAACCAAGCTTACAGAACCGACTTGGAGCGCAATGTCTTGAAAGAATTCATGCCC	5880
QY	6773	CGGTGCTCGACACGTCGAAGAGGAACAACCTCAAACTCAGGTACAGATGATGCCACCG	6832
Db	5881	CGGTGCTCGACACGTCGAAGAGGAACAACCTCAAACTCAGGTACAGATGATGCCACCG	5940
QY	6833	AAGCCAACAAGTAGTACCAGTCTCGTAAAGTAGAAATCAGAAAGCCATAACCACTG	6892
Db	5941	AAGCCAACAAGTAGTACCAGTCTCGTAAAGTAGAAATCAGAAAGCCATAACCACTG	6000
QY	6893	AGCGACTACTGTCAAGACTACGACTGTATTACTCTGCCACAGATCAGCCAGAATGCTATA	6952
Db	6001	AGCGACTACTGTCAAGACTACGACTGTATTACTCTGCCACAGATCAGCCAGAATGCTATA	6060
QY	6953	AGATCACTATCCGAACCAATTGTACTCTCAGTAGCGTACCGGCGAACTACTCCGATCCAC	7012
Db	6061	AGATCACTATCCGAACCAATTGTACTCTCAGTAGCGTACCGGCGAACTACTCCGATCCAC	6120
QY	7013	AGTTCGCTGTAGCTGTCTGTAAACAATCTATCTGCATGGAACCTATCCGACAGTAGACTTT	7072
Db	6121	AGTTCGCTGTAGCTGTCTGTAAACAATCTATCTGCATGGAACCTATCCGACAGTAGACTTT	6180
QY	7073	ATCAGATTACTGACGAGTACGATGCTTACTTGATATGCTAGACGAGACAGTCCGATGCC	7132
Db	6181	ATCAGATTACTGACGAGTACGATGCTTACTTGATATGCTAGACGAGACAGTCCGATGCC	6240
QY	7133	TGGATTACTGCACCTTTCTGCCCGCTAAGCTTGAAGTTACCCGAAAAAATCATGACTATA	7192
Db	6241	TGGATTACTGCACCTTTCTGCCCGCTAAGCTTGAAGTTACCCGAAAAAATCATGACTATA	6300
QY	7193	GAGCCCCGAATATCCGACGTGCGGTTCCATCAGCGATGCAGAACAAGCTACAAAAATGTGC	7252

Db	6301	GAGCCCCGAATATCCGAGTGGCGTTCCATCAGCGATGCAGAACACGCTACAAATGTGC	6360
QY	7253	TCATTGCCGCACTAAAGAAATTGCAACGTCAACGAGATGCCGTGAACCTGCCAACACTGG	7312
Db	6361	TCATTGCCGCACTAAAGAAATTGCAACGTCAACGAGATGCCGTGAACCTGCCAACACTGG	6420
QY	7313	ACTCAGCGACATTCAA TGTGCAATGCTTTGCAAAATATGCATGTAATGACGAGTAATTGGG	7372
Db	6421	ACTCAGCGACATTCAA TGTGCAATGCTTTGCAAAATATGCATGTAATGACGAGTAATTGGG	6480
QY	7373	AGGAGTTCGCTCGAAGCCCAATTAGATTACCATGAGTTTGTCAACCGCATATGTAGCTA	7432
Db	6481	AGGAGTTCGCTCGAAGCCCAATTAGATTACCATGAGTTTGTCAACCGCATATGTAGCTA	6540
QY	7433	GACTGAAAGGCCCTAAGCCCGCCGCACTATTGCAAAAGACGTATATTGGTCCCATTTGC	7492
Db	6541	GACTGAAAGGCCCTAAGCCCGCCGCACTATTGCAAAAGACGTATATTGGTCCCATTTGC	6600
QY	7493	AAGAAGTCCCTATGATAGATTTCGTATGACATGAAAAAGAGACGTGAAGTTACACCAAG	7552
Db	6601	AAGAAGTCCCTATGATAGATTTCGTATGACATGAAAAAGAGACGTGAAGTTACACCAAG	6660
QY	7553	GCACGAAACACACAGAAAGAAAGACCCGAAAGTACAAAGTATCAAGCCGCAAGACCCCTGG	7612
Db	6661	GCACGAAACACACAGAAAGAAAGACCCGAAAGTACAAAGTATCAAGCCGCAAGACCCCTGG	6720
QY	7613	CGACTGCTTACTTAATGCGGGATTCAACCGGAAATTAGTGCGTAGGCTTACGCGCTTGC	7672
Db	6721	CGACTGCTTACTTAATGCGGGATTCAACCGGAAATTAGTGCGTAGGCTTACGCGCTTGC	6780
QY	7673	TTCCAAACATTCAACGCTTTTTCACATGTCGCGGAGATTTTGATGCAATCATAGCAG	7732
Db	6781	TTCCAAACATTCAACGCTTTTTCACATGTCGCGGAGATTTTGATGCAATCATAGCAG	6840
QY	7733	AACACTTCAAGCAAGCGCAACCCGCTACTGAGACGGAATTCGCATCATTCGACAAAGCC	7792
Db	6841	AACACTTCAAGCAAGCGCAACCCGCTACTGAGACGGAATTCGCATCATTCGACAAAGCC	6900
QY	7793	AAGACGACGCTATGCGCTTAACCCGCTGTGATGATCTTGAGGACCTGGGTGTGATCAAC	7852
Db	6901	AAGACGACGCTATGCGCTTAACCCGCTGTGATGATCTTGAGGACCTGGGTGTGATCAAC	6960
QY	7853	CACACTCGACCTTGATCGAGTGCGCCCTTTGGAGAAATATCATCCACCCATCTAACCTACGG	7912
Db	6961	CACACTCGACCTTGATCGAGTGCGCCCTTTGGAGAAATATCATCCACCCATCTAACCTACGG	7020
QY	7913	GTA CTGCTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCTTCACACTTTTGTCA	7972
Db	7021	GTA CTGCTTTTAAATTCGGGGCGATGATGAAATCCGGAATGTTCTTCACACTTTTGTCA	7080
QY	7973	ACACAGTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAACGTCCA	8032
Db	7081	ACACAGTTTGAATGTCGTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAACGTCCA	7140
QY	8033	GATGTCAGCGCTTATTTGGCGCAGCAACATCATATGAGTAGTATCTGCAAAAGAA	8092
Db	7141	GATGTCAGCGCTTATTTGGCGCAGCAACATCATATGAGTAGTATCTGCAAAAGAA	7200
QY	8093	TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAAGTTAAGATCATCGACGCAATCATCG	8152
Db	7201	TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAAGTTAAGATCATCGACGCAATCATCG	7260
QY	8153	GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTGCGTTACTTCCACAG	8212
Db	7261	GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTGCGTTACTTCCACAG	7320
QY	8213	CGTGCCGCGTGGCGGATCCCTGAAAAGGCTGTTAAGTTGGGTAAACCGCTCCACGCCG	8272
Db	7321	CGTGCCGCGTGGCGGATCCCTGAAAAGGCTGTTAAGTTGGGTAAACCGCTCCACGCCG	7380
QY	8273	ACGACGAGCAAGACGAAGACGAGACGCGCTCTGCTAGATGAAACAAAGGCGTGTGTTA	8332

Db	7381	ACGACGAGCAAGACGAAAGACAGAAAGACGCGCTCTGTAGATGAAACAAAGCGGTGTTTA	7440
Qy	8333	GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAAATA	8392
Db	7441	GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAAATA	7500
Qy	8393	TTACACCTGTCTCTACTGGCAATTGAGAACTTTTGCCCAAGCAAAAGACATTCCAAAGCA	8452
Db	7501	TTACACCTGTCTCTACTGGCAATTGAGAACTTTTGCCCAAGCAAAAGACATTCCAAAGCA	7560
Qy	8453	TCAGAGGGGAAATTAAGCATCTCTACGCGTGTCTTAATAGTCAGCATAGTACATTTCAT	8512
Db	7561	TCAGAGGGGAAATTAAGCATCTCTACGCGTGTCTTAATAGTCAGCATAGTACATTTCAT	7620
Qy	8513	CTGACTAATACTACACACCAACCCT	8539
Db	7621	CTGACTAATACTACACACCAACCCT	7647
RESULT 10			
ID	AAD04742	standard; DNA; 9951 BP.	
XX	AC	AAD04742;	
XX	DT	17-JUL-2001 (first entry)	
DE	XX	Alphaviral vector psinReps DNA.	
KW	psinReps5; alphaviral vector; vaccine; therapy; cancer; antiparasitic;		
KW	antimalarial; anticancer; anti-HIV; antiviral; infectious disease;		
KW	Human immunodeficiency virus; HIV; influenza; passive immunisation;		
KW	carcinoma; liver; skin; stomach; ovarian tumour; ds.		
XX	OS	Synthetic.	
PN	WO200130989-A2.		
XX	PD	03-MAY-2001.	
PF	26-OCT-2000; 2000WO-IB001557.		
XX	27-OCT-1999; 99US-0161796P.		
PA	(CYTO-) CYTOS BIOTECHNOLOGY AG.		
PA	(RENN/) RENNER W A.		
PA	(NIEB/) NIEBA L.		
PI	Renner WA, Nieba L;		
XX	WPI; 2001-308631/32.		
PT	Preparing alphaviral vectors with mutations in a selected gene, for use		
PT	as vaccines, particularly against pathogens that mutate rapidly,		
PT	comprises replicating in the presence of a nucleoside analog.		
PS	Claim 4; Fig 4; 103pp; English.		
CC	The present invention relates to a method for preparing viral vectors		
CC	which comprises inserting a gene of interest into an alphaviral vector		
CC	such as pCytRs, psinReps and replicating the vector in the presence of		
CC	5' flucouridine) to produce a modified gene of interest. The replication		
CC	is repeated until the modified gene in 90 % of the vector population		
CC	contain a mutation in the modified gene which is 90-99 % identical with		
CC	the gene of interest. The vector populations are used in vaccines for		
CC	treatment or prevention of a wide variety of infectious diseases (viral		
CC	or parasitic, e.g. human immuno deficiency virus (HIV), influenza,		
CC	Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach		
CC	carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the		
CC	mutant populations will therefore be effective against viral escape		
CC	mutants. Mutagenesis in a eukaryotic cell ensures that expressed proteins		
CC	are correctly glycosylated. Antisera raised against the vaccines can be		

CC	used for passive immunisation. The present DNA sequence is an alphaviral
CC	vector psiRep5. psiRep5 contains nucleic acid which encodes a wild-type
CC	alphaviral replicase. Thus, this replicase in cytopathic and eukaryotic
CC	cells which express it will generally become non-viable within 24 hours
CC	after initiation of expression
XX	
SQ	Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;
	Query Match 89.4%; Score 7637.4; DB 4; Length 9951;
	Best Local Similarity 99.9%; Pred. No. 0;
	Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY	893 ATTGACGGCGTAGTACACACTATTGAATCAAAACGCCAGCCAATTGCACCTACATCAAA
Db	1 ATTGACGGCGTAGTACACACTATTGAATCAAAACGCCAGCCAATTGCACCTACATCAAA
OY	953 TGAGAAGCCAGTAGTAACAAGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTCAA
Db	61 TGAGAAGCCAGTAGTAACAAGTAGACGTAGACCCCCAGAGTCCGTTTGTCGTCAA
OY	1013 AAAAAAGCTTCCCGCAATTGAGGTAGTAGCACACAGGTCACCTCCAAATGACCATGCTA
Db	121 AAAAAAGCTTCCCGCAATTGAGGTAGTAGCACACAGGTCACCTCCAAATGACCATGCTA
OY	1073 ATGCCAGAGCATTTTCGCATCTGCGCCAGTAACTAATCGAGCTGAGGTTCTTACCACAG
Db	181 ATGCCAGAGCATTTTCGCATCTGCGCCAGTAACTAATCGAGCTGAGGTTCTTACCACAG
OY	1133 CGACGATCTTGACATAAGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACAGTATC
Db	241 CGACGATCTTGACATAAGCAGCGCACCGGCTCGTAGAATGTTTTCCGAGCACAGTATC
OY	1193 ATTGTGTCGCCCCCATGCGTAGTCCAGAGAAGACCCGACCCGATGATGAATACGCCAGTA
Db	301 ATTGTGTCGCCCCCATGCGTAGTCCAGAGAAGACCCGACCCGATGATGAATACGCCAGTA
OY	1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAAACAAGAACTGCATGAGAAGATTAAAGATC
Db	361 AACTGGCGGAAAAAGCGTGCAAGATTACAAAACAAGAACTGCATGAGAAGATTAAAGATC
OY	1313 TCCGGAACCGTACTGTGATACGCCCGGATGCTGAAACACCATCGCTCTGCTTTCACAA
Db	421 TCCGGAACCGTACTGTGATACGCCCGGATGCTGAAACACCATCGCTCTGCTTTCACAA
OY	1373 TTACTGCAACATGCGGTGCCGAATATTCGCGTCATGCAAGAACGTATATCAACGCTCCG
Db	481 TTACTGCAACATGCGGTGCCGAATATTCGCGTCATGCAAGAACGTATATCAACGCTCCG
OY	1433 GAACATATCATCATCAGGCTATGAAAGCGGTGCGGACCTGTACTGGAATTGGCTTGACA
Db	541 GAACATATCATCATCAGGCTATGAAAGCGGTGCGGACCTGTACTGGAATTGGCTTGACA
OY	1493 CCACCCAGTTCAATGTTCTCGGCTATGCAAGTTGCTACCTCGTACAAACCAACTGGG
Db	601 CCACCCAGTTCAATGTTCTCGGCTATGCAAGTTGCTACCTCGTACAAACCAACTGGG
OY	1553 CCGACGAGAAAGTCTTGAAGCGCGTAACATCGGACTTTGCAAGCACAAAGCTGAGTGAAG
Db	661 CCGACGAGAAAGTCTTGAAGCGCGTAACATCGGACTTTGCAAGCACAAAGCTGAGTGAAG
OY	1613 GTAGACAGAGAAATTTGTCGATATAGGAAGAGAGTTGAAGCCCGGGTCGGGGTTT
Db	721 GTAGACAGAGAAATTTGTCGATATAGGAAGAGAGTTGAAGCCCGGGTCGGGGTTT
OY	1673 ATTTCTCCGTAGATCGACACTTTATCCAGAACACAGACCAGCTTGACAGAGCTGGCATC
Db	781 ATTTCTCCGTAGATCGACACTTTATCCAGAACACAGACCAGCTTGACAGAGCTGGCATC
OY	1733 TTCCATCGGTGTTCCACTTGAATGGAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG
Db	841 TTCCATCGGTGTTCCACTTGAATGGAAGCAGTCGTACACTTGCCGCTGTGATACAGTGG
OY	1793 TGAAGTGGCAAGGCTACGTAGTGAAGAAATCACCATCAGTCCC GGATCACGGGAGAAA
	1852

Db 901 TGAGTTCGAAAGGCTACGTAGTGAAGAAATCACCATCAGTCCCGGATCACGGAGAAA 960
Qy 1853 CCGTGGGATACCGCGTTACACAAATAGCGAGGGCTTCTGTATGCAAAGTTACTGACA 1912
Db 961 CCGTGGGATACCGCGTTACACAAATAGCGAGGGCTTCTGTATGCAAAGTTACTGACA 1020
Qy 1913 CAGTAAAGAGAAACGGGTATCGTTCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1972
Db 1021 CAGTAAAGAGAAACGGGTATCGTTCCTGTGTGCACGTACATCCCGGCCACCATATGCG 1080
Qy 1973 ATCAGATGACTGGTATATATGGCCACGGATATATCACCTGACGATGCACAAAAATTCTTG 2032
Db 1081 ATCAGATGACTGGTATATATGGCCACGGATATATCACCTGACGATGCACAAAAATTCTTG 1140
Qy 2033 TTGGGCTCAACCGCGAATTGTCATTAACGGTAGGACTAACGAAACCAACACCATGTC 2092
Db 1141 TTGGGCTCAACCGCGAATTGTCATTAACGGTAGGACTAACGAAACCAACACCATGTC 1200
Qy 2093 AAAATTAACCTTCTGCGCATCATAGCACAAGGTTCAAGCAAAATGGCTAAAGAGCGCAAG 2152
Db 1201 AAAATTAACCTTCTGCGCATCATAGCACAAGGTTCAAGCAAAATGGCTAAAGAGCGCAAG 1260
Qy 2153 ATGATCTTGATAACGAGAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
Db 1261 ATGATCTTGATAACGAGAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
Qy 2213 TGTGGCGCTTTCGCACTAAGAAAGTACATTGCTTTATCGCCCACTGGAAACGCAAGCTT 2272
Db 1321 TGTGGCGCTTTCGCACTAAGAAAGTACATTGCTTTATCGCCCACTGGAAACGCAAGCTT 1380
Qy 2273 GCGTAAAGTCCAGCCTCTTTAGCGCTTTTCCCATGTGTCGTATGAGACGACCTCTT 2332
Db 1381 GCGTAAAGTCCAGCCTCTTTAGCGCTTTTCCCATGTGTCGTATGAGACGACCTCTT 1440
Qy 2333 TGCCCATGTGCTGAGGAGAAATGTAACCTGGCATTGCAACCAAGAGAGGAAAAAC 2392
Db 1441 TGCCCATGTGCTGAGGAGAAATGTAACCTGGCATTGCAACCAAGAGAGGAAAAAC 1500
Qy 2393 TGCTGAGGTCTCGAGGAATTAGTCATGAGGCCAAGGCTGCTTTGAGGATGCTCAGG 2452
Db 1501 TGCTGAGGTCTCGAGGAATTAGTCATGAGGCCAAGGCTGCTTTGAGGATGCTCAGG 1560
Qy 2453 AGGAAGCCAGAGCGGAGAAAGCTCCGAGAAACACTTCCACCATTAGTGGCAGACAAAGCA 2512
Db 1561 AGGAAGCCAGAGCGGAGAAAGCTCCGAGAAACACTTCCACCATTAGTGGCAGACAAAGCA 1620
Qy 2513 TCGAGGAGCCGCGAGAAAGTGTCTGCGAAGTGGAGGGGCTCCAGGGGACATCGGAGCAG 2572
Db 1621 TCGAGGAGCCGCGAGAAAGTGTCTGCGAAGTGGAGGGGCTCCAGGGGACATCGGAGCAG 1680
Qy 2573 CATTAGTTGAAACCCCGCGGTCACGTAAGGATATACCTCAAGCAAAATGACCCGTATGA 2632
Db 1681 CATTAGTTGAAACCCCGCGGTCACGTAAGGATATACCTCAAGCAAAATGACCCGTATGA 1740
Qy 2633 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAAATGCCAACTCGACACAG 2692
Db 1741 TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAAATGCCAACTCGACACAG 1800
Qy 2693 CGCACCCTAGCAGATCAGGTTAAGTATATAACACACTCCGGAAGATCAGGAAGGTACG 2752
Db 1801 CGCACCCTAGCAGATCAGGTTAAGTATATAACACACTCCGGAAGATCAGGAAGGTACG 1860
Qy 2753 CCGTGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 2812
Db 1861 CCGTGAACCATACGACGCTAAAGTACTGATGCCAGCAGGAGGTGCCGTACCATGGCCAG 1920
Qy 2813 AATTCTAGCACTGAGTGAGAGCGCCAGCTTAGTGTAACAAGAAAGAGATTGTGAACC 2872
Db 1921 AATTCTAGCACTGAGTGAGAGCGCCAGCTTAGTGTAACAAGAAAGAGATTGTGAACC 1980
Qy 2873 GCAAACTATACCATTTGCCATGCTGGCCCCGCCAAGAATACAGAAAGAGCAGTACA 2932

Db 1981 GCAAACTATACCATTTGCCATGCTAGGCCCGCCCAAGAAATACAGAAAGAGCAGTACA 2040
Qy 2933 AGGTTACAAAGCGAGAGCTTTCAGAAACAGAGTACGTTTGTGACGTGGACAAAGAGCGTT 2992
Db 2041 AGGTTACAAAGCGAGAGCTTTCAGAAACAGAGTACGTTTGTGACGTGGACAAAGAGCGTT 2100
Qy 2993 GCGTTAAGAAAGAAAGCCTCAGGCTGTGCTCTCTCGGAGAACTGACCAACCTCCCT 3052
Db 2101 GCGTTAAGAAAGAAAGCCTCAGGCTGTGCTCTCTCGGAGAACTGACCAACCTCCCT 2160
Qy 3053 ATCATGAGCTAGCTCTGAGGGACTGAAGACCCGACCTGCGGTCCGTACAAGGTGAAA 3112
Db 2161 ATCATGAGCTAGCTCTGAGGGACTGAAGACCCGACCTGCGGTCCGTACAAGGTGAAA 2220
Qy 3113 CAATAGAGTATAGGACACCGGGGTCCGGCAAGTCAAGTATATCAAGTCAACTGTCA 3172
Db 2221 CAATAGAGTATAGGACACCGGGGTCCGGCAAGTCAAGTATATCAAGTCAACTGTCA 2280
Qy 3173 CGGCAAGAGATCTGTACACCGGAAAGAAAGAAATTTGCGGAATTGAGGCCGACG 3232
Db 2281 CGGCAAGAGATCTGTACACCGGAAAGAAAGAAATTTGCGGAATTGAGGCCGACG 2340
Qy 3233 TGTAAAGACTGAGGGGTATGCAATTACGTGGAAGACAGTAAATTCGGTTATGCTCAACG 3292
Db 2341 TGTAAAGACTGAGGGGTATGCAATTACGTGGAAGACAGTAAATTCGGTTATGCTCAACG 2400
Qy 3293 GATGCCACAAAGCCGTAGAAAGTCTGTACGTTGACGAAGCGTTCGCGTCCACGACGAG 3352
Db 2401 GATGCCACAAAGCCGTAGAAAGTCTGTACGTTGACGAAGCGTTCGCGTCCACGACGAG 2460
Qy 3353 CACTACTTGCTGTATGCTATCGTCAGGCCCCGCAAGAGTAGTACTATGCGAGACC 3412
Db 2461 CACTACTTGCTGTATGCTATCGTCAGGCCCCGCAAGAGTAGTACTATGCGAGACC 2520
Qy 3413 CCAATGCAATGCGGATTTCTCAACATGATGCAACTAAAGTACATTTCAATCACCCTGAAA 3472
Db 2521 CCAATGCAATGCGGATTTCTCAACATGATGCAACTAAAGTACATTTCAATCACCCTGAAA 2580
Qy 3473 AAGACATATGCAACCAAGACATTTCTAACAAGTATATCTCCCGCGTTGCAACAGCCAGTTA 3532
Db 2581 AAGACATATGCAACCAAGACATTTCTAACAAGTATATCTCCCGCGTTGCAACAGCCAGTTA 2640
Qy 3533 CAGCTATTGTATCGACACTGCAATTCGATGGAAGATGAAAAACCAAGAACCCGTCAAGA 3592
Db 2641 CAGCTATTGTATCGACACTGCAATTCGATGGAAGATGAAAAACCAAGAACCCGTCAAGA 2700
Qy 3593 AGAATTTGAATCGATATTAACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCTGTA 3652
Db 2701 AGAATTTGAATCGATATTAACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCTGTA 2760
Qy 3653 CATGTTCCGGCGGTGGTAAAGCAATTGCAAAATCGATCCCGGACATGAAGTAATGA 3712
Db 2761 CATGTTCCGGCGGTGGTAAAGCAATTGCAAAATCGATCCCGGACATGAAGTAATGA 2820
Qy 3713 CAGCCCGGGCTCACAAAGGGCTAACGAAAAAGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db 2821 CAGCCCGGGCTCACAAAGGGCTAACGAAAAAGAGTGTATGCCGTCCGGCAAAAAGTCA 2880
Qy 3773 ATGAAAAACCACTGTACGCGATCACAATCAGAGCATGTGAACGTGTGCTCACCCGACTG 3832
Db 2881 ATGAAAAACCACTGTACGCGATCACAATCAGAGCATGTGAACGTGTGCTCACCCGACTG 2940
Qy 3833 AGGACAGGCTAGTGTGAAAACTTGCAGGGCGACCCATGGAATTAAGCAGCCCACTAACA 3892
Db 2941 AGGACAGGCTAGTGTGAAAACTTGCAGGGCGACCCATGGAATTAAGCAGCCCACTAACA 3000
Qy 3893 TACTTAAAGGAACTTTCAGGCTACTATAGAGACTGGAGCTGAACACAGGAATAA 3952
Db 3001 TACTTAAAGGAACTTTCAGGCTACTATAGAGACTGGAGCTGAACACAGGAATAA 3060
Qy 3953 TTGCTGCAATTAACAGCCCACTCCCGTGCCAATCCGTTCACTGCAAGACCAACGTTT 4012
Db 3061 TTGCTGCAATTAACAGCCCACTCCCGTGCCAATCCGTTCACTGCAAGACCAACGTTT 3120

QY 4013 GCTGGCGAAAGCATTTGGAACCGATACAGCCGCGGATCGTACTTACCGGTGCC 4072
 |||||
 Db 3121 GCTGGCGAAAGCATTTGGAACCGATACAGCCGCGGATCGTACTTACCGGTGCC 3180
 QY 4073 AGTGAGCGAAGCTGTTCACACAGTTTGGCGATGACAACACCATTCGGCATTTACGCCCT 4132
 |||||
 Db 3181 AGTGAGCGAAGCTGTTCACACAGTTTGGCGATGACAACACCATTCGGCATTTACGCCCT 3240
 QY 4133`TAGACGTAATTGGCATTTAAGTTTTCGGCATGGAATTGACAAGCGGACTGTTTCTTAAC 4192
 |||||
 Db 3241 TAGACGTAATTGGCATTTAAGTTTTCGGCATGGAATTGACAAGCGGACTGTTTCTTAAC 3300
 QY 4193 AGAGCATCCCACTAACGTACCATCCCGCGATTTCAGCGAGCGCGGTAGCTATTGGGACA 4252
 |||||
 Db 3301 AGAGCATCCCACTAACGTACCATCCCGCGATTTCAGCGAGCGCGGTAGCTATTGGGACA 3360
 QY 4253 ACAGCCCGAAGAACCCGCAAGTATGGGTACGATCAGCCATTGCCCGCAACTCTCCCGTA 4312
 |||||
 Db 3361 ACAGCCCGAAGAACCCGCAAGTATGGGTACGATCAGCCATTGCCCGCAACTCTCCCGTA 3420
 QY 4313 GATTTCGGGTGTTCCAGCTAGCTGGGAAGGACACAACTTGATTGTCAGCGGGAGAA 4372
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 Db 3421 GATTTCGGGTGTTCCAGCTAGCTGGGAAGGACACAACTTGATTGTCAGCGGGAGAA 3480
 QY 4373 CCAGAGTTATCTCTGCACACGATTAACCTGGTCCGGTGAACCCGCAATCTTCTCAAGCCT 4432
 |||||
 Db 3481 CCAGAGTTATCTCTGCACACGATTAACCTGGTCCGGTGAACCCGCAATCTTCTCAAGCCT 3540
 QY 4433 TAGTCCCCGAGTACAAGAGAAGCAACCCGCGCGTCAAAAAATTCTTGAACCAAGTTCA 4492
 |||||
 Db 3541 TAGTCCCCGAGTACAAGAGAAGCAACCCGCGCGTCAAAAAATTCTTGAACCAAGTTCA 3600
 QY 4493 AACACCACTCAGTACTTGTGTATCAGAGAAAAAATTGAAGCTCCCGTAAAGAAATCG 4552
 |||||
 Db 3601 AACACCACTCAGTACTTGTGTATCAGAGAAAAAATTGAAGCTCCCGTAAAGAAATCG 3660
 QY 4553 AATGATCGCCCCGATTTGGCATAGCCGGTGCATAAGAACTACAACCTGGCTTCCGGT 4612
 |||||
 Db 3661 AATGATCGCCCCGATTTGGCATAGCCGGTGCATAAGAACTACAACCTGGCTTCCGGT 3720
 QY 4613 TTCCGCGCAGGCAAGGTAACGACCTGGTTCATCAACATTGGAATTAATAAGAAACC 4672
 |||||
 Db 3721 TTCCGCGCAGGCAAGGTAACGACCTGGTTCATCAACATTGGAATTAATAAGAAACC 3780
 QY 4673 ACCACTTTACGAGTGCAGAAAGCAATGCGGCACTTAAAAACCCTTCCGGTTCGGCCC 4732
 |||||
 Db 3781 ACCACTTTACGAGTGCAGAAAGCAATGCGGCACTTAAAAACCCTTCCGGTTCGGCCC 3840
 QY 4733 TGAATTGTTTAACTCAGAGAGCACCTCGTGTGAAGTCCCTATGGCTAGCGCGACCGCA 4792
 |||||
 Db 3841 TGAATTGCTTAACTCAGAGAGCACCTCGTGTGAAGTCCCTATGGCTAGCGCGACCGCA 3900
 QY 4793 ACAGTGAGAGCTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAAGGTGTCTGACCGAGAC 4852
 |||||
 Db 3901 ACAGTGAGAGCTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAAGGTGTCTGACCGAGAC 3960
 QY 4853 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCGACAACTAGACAACAGCC 4912
 |||||
 Db 3961 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCGACAACTAGACAACAGCC 4020
 QY 4913 GTACACGGCAATTCAACCCGCAACCATCTGAATTGCGTGAATTCGTCGTTAGAGGTA 4972
 |||||
 Db 4021 GTACACGGCAATTCAACCCGCAACCATCTGAATTGCGTGAATTCGTCGTTAGAGGTA 4080
 QY 4973 CAAGAGATGAGTTGAGACCGCGCGTCAATACCGCAACCAAAAGGAGAAATTTGCTGACT 5032
 |||||
 Db 4081 CAAGAGATGAGTTGAGACCGCGCGTCAATACCGCAACCAAAAGGAGAAATTTGCTGACT 4140
 QY 5033 GTCAAGAGGAAGAGTTGTCAACGACAGCCCAATCCGCTGGGTAGACCAAGGAGAGTCT 5092
 |||||
 Db 4141 GTCAAGAGGAAGAGTTGTCAACGACAGCCCAATCCGCTGGGTAGACCAAGGAGAGTCT 4200

QY 5093 GCCGTGCCATCTATAACGTTGGCCGACCAAGTTTACCAGATTACGCCACGGAGACAGGCA 5152
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 Db 4201 GCCGTGCCATCTATAACGTTGGCCGACCAAGTTTACCAGATTACGCCACGGAGACAGGCA 4260
 QY 5153 CCGCAAGATGACTGTGTGCTAGGAAAGAAAGTATCCACGCGGTGGCGCTGATTCC 5212
 |||||
 Db 4261 CCGCAAGATGACTGTGTGCTAGGAAAGAAAGTATCCACGCGGTGGCGCTGATTCC 4320
 QY 5213 GGAAGCACCCAGAAAGCAGAAAGCTTGAATTGCTACAAAAAGCTTACAGTGCAGTGCCAG 5272
 |||||
 Db 4321 GGAAGCACCCAGAAAGCAGAAAGCTTGAATTGCTACAAAAAGCTTACAGTGCAGTGCCAG 4380
 QY 5273 ACTTAGTAATGAACATTAACATCAAGTGTGCGCATTTCCACTGCTATCTACAGGCATTT 5332
 |||||
 Db 4381 ACTTAGTAATGAACATTAACATCAAGTGTGCGCATTTCCACTGCTATCTACAGGCATTT 4440
 QY 5333 ACGAGCCGGAAAAAGACCCGCTTGAAGTATCACTTAAGTGTGACAAACCGCGCTAGACA 5392
 |||||
 Db 4441 ACGAGCCGGAAAAAGACCCGCTTGAAGTATCACTTAAGTGTGACAAACCGCGCTAGACA 4500
 QY 5393 GAACTGACGCGGACGTAAACCATCTATTGCTGATTAAGAAAGTGGAAGAAAGAAATCGACG 5452
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 Db 4501 GAACTGACGCGGACGTAAACCATCTATTGCTGATTAAGAAAGTGGAAGAAAGAAATCGACG 4560
 QY 5453 CGGCACTCCAACTTAAAGAGTCTGTAACAGAGCTGAAGATGAAGATGAGATCGACG 5512
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 Db 4561 CGGCACTCCAACTTAAAGAGTCTGTAACAGAGCTGAAGATGAAGATGAGATCGACG 4620
 QY 5513 ATGAGTTAGTATGATTTCATCCAGACAGTTGCTTGAAGGAAGAAAGGAATTCAAGTACTA 5572
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 Db 4621 ATGAGTTAGTATGATTTCATCCAGACAGTTGCTTGAAGGAAGAAAGGAATTCAAGTACTA 4680
 QY 5573 CAAAAGAAAATTGTAATTCGTAATTCGAAGGCAACCAATTCCATCAAGCAACAAAAGACA 5632
 |||||
 Db 4681 CAAAAGAAAATTGTAATTCGTAATTCGAAGGCAACCAATTCCATCAAGCAACAAAAGACA 4740
 QY 5633 TGGCGGAGATAAGGTCCTGTTCCCTTAATGACAGGAAAGTAATGAACAATGTGTGCCT 5692
 |||||
 Db 4741 TGGCGGAGATAAGGTCCTGTTCCCTTAATGACAGGAAAGTAATGAACAATGTGTGCCT 4800
 QY 5693 ACATATTGGGTGAGACCATGGAAGCAATCCGAAAAAGTGCCCGGTGCAACATAACCCGT 5752
 |||||
 Db 4801 ACATATTGGGTGAGACCATGGAAGCAATCCGAAAAAGTGCCCGGTGCAACATAACCCGT 4860
 QY 5753 CGTCTAGCCCGCCAAACGTTGCCGTGCTTGCATGTATGCCATGACGCCAGAAAGGG 5812
 |||||
 Db 4861 CGTCTAGCCCGCCAAACGTTGCCGTGCTTGCATGTATGCCATGACGCCAGAAAGGG 4920
 QY 5813 TCCACAGACTTGAAGCAATTAACGTCAAAAGAGTTACAGTATGCTCTCCACCCCCCTTC 5872
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 Db 4921 TCCACAGACTTGAAGCAATTAACGTCAAAAGAGTTACAGTATGCTCTCTCCACCCCCCTTC 4980
 QY 5873 CTAAGCACAATAATTAAAGATGTTCAAGAGTTCAAGTGCAGGAAAGTACTGCTGTTAATC 5932
 |||||
 Db 4981 CTAAGCACAATAATTAAAGATGTTCAAGAGTTCAAGTGCAGGAAAGTACTGCTGTTAATC 5040
 QY 5933 CGCACACTCCCGCATTCGTTCCCGCCGTAAGTACATAGAAGTGCCAGAAAGCCTTACCG 5992
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 Db 5041 CGCACACTCCCGCATTCGTTCCCGCCGTAAGTACATAGAAGTGCCAGAAAGCCTTACCG 5100
 QY 5993 CTCCTCTGACAGAGCCGAGAGAGGCCCCCGAAGTTGTAGCGACACCGTCAACCATCTACAG 6052
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 Db 5101 CTCCTCTGACAGAGCCGAGAGAGGCCCCCGAAGTTGTAGCGACACCGTCAACCATCTACAG 5160
 QY 6053 CTGATAACACCTCGCTTGATGTCAACAGACATCTCACTGGATATGATGACAGTAGCGAAG 6112
 |||||
 Db 5161 CTGATAACACCTCGCTTGATGTCAACAGACATCTCACTGGATATGATGACAGTAGCGAAG 5220
 QY 6113 GCTCACTTTTTCGAGCTTTAGCGGATCGGCAACTTATTAAGTATGACAGAGTGTGT 6172
 |||||
 Db 5221 GCTCACTTTTTCGAGCTTTAGCGGATCGGCAACTTATTAAGTATGACAGAGTGTGT 5280
 QY 6173 CGTCAGGACCTAGTTCACTAGAGATAGTAGACCGAAAGGAGGTGTGTGCTGACGTTTC 6232

Db	5281	CGTCAGGACCTAGTTCACCTAGAGATAGTAGACCCGAAGGACAGGTGTGTGGCTGACGTTCC	5340
Qy	6233	ATGCCGTCCAAGAGCCTGCCCCCTATTCCACCCGCCAAGGCTAAAGAAAGATGGCCCCCTGG	6292
Db	5341	ATGCCGTCCAAGAGCCTGCCCCCTATTCCACCCGCCAAGGCTAAAGAAAGATGGCCCCCTGG	5400
Qy	6293	CAGCGGCAAGAAAAGAGCCCACTCCACCCGCCAAGCAATAGCTCTGAGTCCCTCCACTCT	6352
Db	5401	CAGCGGCAAGAAAAGAGCCCACTCCACCCGCCAAGCAATAGCTCTGAGTCCCTCCACTCT	5460
Qy	6353	CTTTTGGTGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCCCAGG	6412
Db	5461	CTTTTGGTGGGTATCCATGTCCCTCGGATCAATTTTCGACGGAGAGACGGCCCCCAGG	5520
Qy	6413	CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCTTGTCTTTCGATCGTTTT	6472
Db	5521	CAGCGGTACAACCCCTGGCAACAGGCCCCACGGATGTGCTTGTCTTTCGATCGTTTT	5580
Qy	6473	CCGACGGAGAGATTGATGAGCTGAGCCCGCAGAGTAACTGAGTCCGAACCCGTCGTTTTG	6532
Db	5581	CCGACGGAGAGATTGATGAGCTGAGCCCGCAGAGTAACTGAGTCCGAACCCGTCGTTTTG	5640
Qy	6533	GATCATTTGAACCCGGGCCAAGTGAACTCAATTATATCGTCCCGATCAGCCGTAATCTTTT	6592
Db	5641	GATCATTTGAACCCGGGCCAAGTGAACTCAATTATATCGTCCCGATCAGCCGTAATCTTTT	5700
Qy	6593	CACCTACGCAAGCAGAGACGTAGAAGCAGAGACAGAGAGCTGAATACTGACTTAAACGGGG	6652
Db	5701	CACCTACGCAAGCAGAGACGTAGAAGCAGAGACAGAGAGCTGAATACTGACTTAAACGGGG	5760
Qy	6653	TAGTGGGTACATATTTTCGACGGAACAGAGCCCTGGGCACTTGCAAAAAGAAAGTCCGTT	6712
Db	5761	TAGTGGGTACATATTTTCGACGGAACAGAGCCCTGGGCACTTGCAAAAAGAAAGTCCGTT	5820
Qy	6713	TGCAGAACCAGCTTACAGAACCGACCTTGAGCGCAATGTCTGAAAAGAAATTCATGCC	6772
Db	5821	TGCAGAACCAGCTTACAGAACCGACCTTGAGCGCAATGTCTGAAAAGAAATTCATGCC	5880
Qy	6773	CGGTGCTCGACACGTGCAAGAGAGAAACAACCTCAAACTCAGGTACAGATGATGCCACCG	6832
Db	5881	CGGTGCTCGACACGTGCAAGAGAGAAACAACCTCAAACTCAGGTACAGATGATGCCACCG	5940
Qy	6833	AAGCCAACAAAAGTAGGTACGAGTCTCGTAAAGTAGAATAACGAAAGCCATTAACCACTG	6892
Db	5941	AAGCCAACAAAAGTAGGTACGAGTCTCGTAAAGTAGAATAACGAAAGCCATTAACCACTG	6000
Qy	6893	AGCGACTACTGTACGAGACTGAGACTGTATTAACCTCTGCCACAGATCAGCCAGAAATGCTATA	6952
Db	6001	AGCGACTACTGTACGAGACTGAGACTGTATTAACCTCTGCCACAGATCAGCCAGAAATGCTATA	6060
Qy	6953	AGATCACTTATCCGAAACCAATGTACTCCAGTAGCGTACGGGCAACTACTCCGATCCAC	7012
Db	6061	AGATCACTTATCCGAAACCAATGTACTCCAGTAGCGTACGGGCAACTACTCCGATCCAC	6120
Qy	7013	AGTTGCTGTAGCTGTCTGTAAACAATATCTGCATGAGAACTATCCGACAGTAGACTTT	7072
Db	6121	AGTTGCTGTAGCTGTCTGTAAACAATATCTGCATGAGAACTATCCGACAGTAGACTTT	6180
Qy	7073	ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCCGATGCC	7132
Db	6181	ATCAGATTACTGACGAGTACGATGCTTACTTGGATATGGTAGACGAGACAGTCCGATGCC	6240
Qy	7133	TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTAACCGAAAAACATGAGTATA	7192
Db	6241	TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTAACCGAAAAACATGAGTATA	6300
Qy	7193	GAGCCCCGAATATCCGACAGTGGGTTCATCAGCGATGCAACAACGCTACAAATATGTC	7252
Db	6301	GAGCCCCGAATATCCGACAGTGGGTTCATCAGCGATGCAACAACGCTACAAATATGTC	6360
Qy	7253	TCAATTCCGCACTAAAAGAAATTGCAACGTACAGCAGATGGGTGAAGTGCACCAACTGG	7312

Db	6361	TCATTGCCGCCAACTMAAAGAAATTGCAACGTCACGCAGATGCGTGAATCGCAACACTGG	6420
Qy	7313	ACTCAGCGACATTCAATGTCGAATGCTTTGAAAATATGCATGTAAATGACGAGTATTGGG	7372
Db	6421	ACTCAGCGACATTCAATGTCGAATGCTTTGAAAATATGCATGTAAATGACGAGTATTGGG	6480
Qy	7373	AGGAGTTGCTCGGAAGCCAAATTAGATTACCACTGAGTTTGTCACCGCATAATGTAAGTA	7432
Db	6481	AGGAGTTGCTCGGAAGCCAAATTAGATTACCACTGAGTTTGTCACCGCATAATGTAAGTA	6540
Qy	7433	GACTGAAAGGCCCTAAGCGCCGCCACTATTGCAAAAGACGTATAATTTGGTCCCATTGC	7492
Db	6541	GACTGAAAGGCCCTAAGCGCCGCCACTATTGCAAAAGACGTATAATTTGGTCCCATTGC	6600
Qy	7493	AAGAAGTGCCTATGGATAGATTGTCATGACATGAAAAGAGACGTGAAAGTTACACCAG	7552
Db	6601	AAGAAGTGCCTATGGATAGATTGTCATGACATGAAAAGAGACGTGAAAGTTACACCAG	6660
Qy	7553	GCACGAAACACACAGAAAGAACCCGAAAGTACAAAGTATCAAGCCGCAGAACCCCTGG	7612
Db	6661	GCACGAAACACACAGAAAGAACCCGAAAGTACAAAGTATCAAGCCGCAGAACCCCTGG	6720
Qy	7613	CGACTGCTTACTTATGCGGGAATTCACCGGAAATTAGTCGTAGGCTTACCGCGCTTGGC	7672
Db	6721	CGACTGCTTACTTATGCGGGAATTCACCGGAAATTAGTCGTAGGCTTACCGCGCTTGGC	6780
Qy	7673	TTCCAAACATTCACACGCTTTTGAATGTCGCGCGAGATTTTGATGCAATCATAGCAG	7732
Db	6781	TTCCAAACATTCACACGCTTTTGAATGTCGCGCGAGATTTTGATGCAATCATAGCAG	6840
Qy	7733	AACACTTCAAGCAAGGCGACCCCGTACTGAGACCGATATCGCATCATTCGACAAAAGCC	7792
Db	6841	AACACTTCAAGCAAGGCGACCCCGTACTGAGACCGATATCGCATCATTCGACAAAAGCC	6900
Qy	7793	AAGACGACGCTATGGCGTTAACCGGCTCTGATGATCTTGAGAGAACCTGGGTGTCATCAAC	7852
Db	6901	AAGACGACGCTATGGCGTTAACCGGCTCTGATGATCTTGAGAGAACCTGGGTGTCATCAAC	6960
Qy	7853	CACCTACTGCACTTGATCGAGTGCCTTTTGAGAAATATCATCCACCATCTTACTACGG	7912
Db	6961	CACCTACTGCACTTGATCGAGTGCCTTTTGAGAAATATCATCCACCATCTTACTACGG	7020
Qy	7913	GTACTCGTTTAAATTCCGGGCGATGATGAAATCCGGAATGTTCTCACACTTTTGTCA	7972
Db	7021	GTACTCGTTTAAATTCCGGGCGATGATGAAATCCGGAATGTTCTCACACTTTTGTCA	7080
Qy	7973	ACACAGTTTGAATGTCGTTATGCGCAGACAGACTACTGAAAGCGGCTTAAACGTCCA	8032
Db	7081	ACACAGTTTGAATGTCGTTATGCGCAGACAGACTACTGAAAGCGGCTTAAACGTCCA	7140
Qy	8033	GATGTGCAGCGTTTCAATTGGCGACGACAACATCATATCATGGAAGTAGTATCTGACAAAAGAA	8092
Db	7141	GATGTGCAGCGTTTCAATTGGCGACGACAACATCATATCATGGAAGTAGTATCTGACAAAAGAA	7200
Qy	8093	TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAAGTTAAGATCATCGACGCAGTCATCG	8152
Db	7201	TGGCTGAGAGGTGCGCCACCTGGCTCAACATGGAAGTTAAGATCATCGACGCAGTCATCG	7260
Qy	8153	GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG	8212
Db	7261	GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTCGGTTACTTCCACAG	7320
Qy	8213	CGTGCCGCGTGGCGGATCCCTGTAAGGCTGTTAAGTTGGGTAACCGCTCCAGCCG	8272
Db	7321	CGTGCCGCGTGGCGGATCCCTGTAAGGCTGTTAAGTTGGGTAACCGCTCCAGCCG	7380
Qy	8273	ACGACGAGCAAGACGAAGACGAAGACGCGCTCTGCTAGATGAAAACAAGCGTGGTTTA	8332
Db	7381	ACGACGAGCAAGACGAAGACGAAGACGCGCTCTGCTAGATGAAAACAAGCGTGGTTTA	7440
Qy	8333	GAGTAGGTATTAACAGGCACTTTAGAGTGGCCGTGACGACCCGGTATGAGGTAGACATA	8392
Db	7441	GAGTAGGTATTAACAGGCACTTTAGAGTGGCCGTGACGACCCGGTATGAGGTAGACATA	7500

Db 1081 ATCAGATGACTGGTATTAATGCGCACGGATATATCACTGACGATGCACAAAACTTCTGG 1140
Qy 2033 TTGGGCTCAACCAAGCGAATTGTCAATTAACGGTAGGACTAAAGAAACCAACCATGTC 2092
Db 1141 TTGGGCTCAACCAAGCGAATTGTCAATTAACGGTAGGACTAAAGAAACCAACCATGTC 1200
Qy 2093 AAAATTACCTTCTGCGCATCATAGCACAAAGGTTCAACAAATGGGCTAAAGAGCGCAAG 2152
Db 1201 AAAATTACCTTCTGCGCATCATAGCACAAAGGTTCAACAAATGGGCTAAAGAGCGCAAG 1260
Qy 2153 ATGATCTTGATTAACGAGAAATGCTGGTACTAGAAACGCAAGCTTACGTATGCTGCT 2212
Db 1261 ATGATCTTGATTAACGAGAAATGCTGGTACTAGAAACGCAAGCTTACGTATGCTGCT 1320
Qy 2213 TGTGGCGGTTTGGCACTAAGAAAGTACATTCGTTTATCGCCCACTGGAACGCAACCT 2272
Db 1321 TGTGGCGGTTTGGCACTAAGAAAGTACATTCGTTTATCGCCCACTGGAACGCAACCT 1380
Qy 2273 GCGTAAAGTCCCAAGCCTCTTTAGCGCTTTCCCATGTGTCCTGTAAGACGACCTCTT 2332
Db 1381 GCGTAAAGTCCCAAGCCTCTTTAGCGCTTTTCCCATGTGTCCTGTAAGACGACCTCTT 1440
Qy 2333 TGCCCATGTGCTGAGGCGAGAAATTGAATGGCATTTGCAACCAAGAGGAGGAAAAAC 2392
Db 1441 TGCCCATGTGCTGAGGCGAGAAATTGAATGGCATTTGCAACCAAGAGGAGGAAAAAC 1500
Qy 2393 TGCTGACGCTCTGGAGGAATTAGTCATGAGGCGCAAGGCTGTTTGAAGATGCTCAGG 2452
Db 1501 TGCTGACGCTCTGGAGGAATTAGTCATGAGGCGCAAGGCTGTTTGAAGATGCTCAGG 1560
Qy 2453 AGGAAGCCAGAGCGGAGAAAGCTCCGAGAGCACTTCCACATTAGTGGCAGACAAAGCA 2512
Db 1561 AGGAAGCCAGAGCGGAGAAAGCTCCGAGAGCACTTCCACATTAGTGGCAGACAAAGCA 1620
Qy 2513 TCGAGGCGAGCGCAGAAAGTTGTCTGCGAAATGGAGGGGCTCCAGGCGGACATCGAGCAG 2572
Db 1621 TCGAGGCGAGCGCAGAAAGTTGTCTGCGAAATGGAGGGGCTCCAGGCGGACATCGAGCAG 1680
Qy 2573 CATTAGTTGAAACCCCGCGGCTACGTTAAGGATTAATACCTCAAGCAATGACCGTATGA 2632
Db 1681 CATTAGTTGAAACCCCGCGGCTACGTTAAGGATTAATACCTCAAGCAATGACCGTATGA 1740
Qy 2633 TCGGACAGTATATCGTTGTCTGCGCAAACTGTGCTGAAGAATGCCAACTCGCACAG 2692
Db 1741 TCGGACAGTATATCGTTGTCTGCGCAAACTGTGCTGAAGAATGCCAACTCGCACAG 1800
Qy 2693 CGCACCCGCTAGCAGATCAGGTTAAGTATCAACACACTCCGGAAGATCAGGAAGTAGC 2752
Db 1801 CGCACCCGCTAGCAGATCAGGTTAAGTATCAACACACTCCGGAAGATCAGGAAGTAGC 1860
Qy 2753 CGGTGAACCATACGAGCGCTAAAGTACTGATGCCAGCAGAGGTCGGTACCATGCGCAG 2812
Db 1861 CGGTGAACCATACGAGCGCTAAAGTACTGATGCCAGCAGAGGTCGGTACCATGCGCAG 1920
Qy 2813 AATTCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAAAGAAAGAGAGTTGTGAACC 2872
Db 1921 AATTCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAAAGAAAGAGAGTTGTGAACC 1980
Qy 2873 GCAAACTATACCACTTGGCATGTGCGCCCGCCCAAGAATACAGAAAGAGCAGTACA 2932
Db 1981 GCAAACTATACCACTTGGCATGTGCGCCCGCCCAAGAATACAGAAAGAGCAGTACA 2040
Qy 2933 AGGTACAAGGAGAGGCTTGCAAAACAGAGTACGTTTGAAGTGAAGGCTT 2992
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Qy 2993 GCGTTAAGAGGAAGAGCCTCAGGTCTGCTCTCGGAGAACTGACCAACCTCCCT 3052
Db 2101 GCGTTAAGAGGAAGAGCCTCAGGTCTGCTCTCGGAGAACTGACCAACCTCCCT 2160
Qy 3053 ATCATGAGCTAGCTCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTACAAAGTCAAAA 3112

Db 2161 ATCATGAGCTAGCTCTGAGAGGACTGAAGACCCGACCTGCGGTCCCGTACAAAGTCAAAA 2220
Qy 3113 CAATAGAGTGTATAGGCACACCGGGGTTCGGCAAGTCAAGTATTAACAAGTCAACTGTCA 3172
Db 2221 CAATAGAGTGTATAGGCACACCGGGGTTCGGCAAGTCAAGTATTAACAAGTCAACTGTCA 2280
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Qy 3233 TGCTAAGACTGAGGGGTATGAGATTAAGTGAAGACAGTAGATTGCGTTATGCTCAACG 3292
Db 2341 TGCTAAGACTGAGGGGTATGAGATTAAGTGAAGACAGTAGATTGCGTTATGCTCAACG 2400
Qy 3293 GATGCCACAAAGCCGTAAGAGTGTGTACGTTGACGAAAGCGTTGCGTGCACGACAGAG 3352
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Db 2461 CACTACTTGCCCTGATTTGCTATCGTCAAGGCCCGCAAGAGGTACTATGCGGAGACC 2520
Qy 3413 CCATGCAATGCGGATTTCTTCAACATGATGCAACTTAAAGTTAATTCAATCAACCTGAAA 3472
Db 2521 CCATGCAATGCGGATTTCTTCAACATGATGCAACTTAAAGTTAATTCAATCAACCTGAAA 2580
Qy 3473 AAGACATATGCACCAAGACATTTCTACAAGTATATCTCCGCGGCTTGACACACAGCCAGTTA 3532
Db 2581 AAGACATATGCACCAAGACATTTCTACAAGTATATCTCCGCGGCTTGACACACAGCCAGTTA 2640
Qy 3533 CAGCTATTGTATGCACACTGCACTTAAGATGAAGATGAACCAAGAACCCGTGCAAGA 3592
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Qy 3593 AGAATTTGAATCGATTAACAGGGGCCACAAAGCCGAAGCCAGGGATATCATCTGTA 3652
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Qy 3653 CATGTTTCCGCGGTGGTTAAGCAATTGCAAAATGCAATTCGCGACATGAAGTAATGA 3712
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Db 2821 CAGCCGCGGCTCAACAAGGCTAACCAAGAAAGAGTATGCCGTCCGGCAAAAAGTCA 2880
Qy 3773 ATGAAACCACCTGTACCGGATCACATCAGAGCATGTGAACGTGTGCTCACCCGCACTG 3832
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Qy 3833 AGGACAGGCTAGTGTGAAAACTTGACAGGGCGAACCAATGATTAAGCAGCCCACTAACA 3892
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Qy 4013 GCTGGCGGAAAGCATTTGGAACCGATACTAGCCACGGCGGTAATGTAATTAACCGTTGCC 4072
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Qy 4073 AGTGAAGCAACTGTTCCACAAGTTTGCGGATGACAAACCAATTCGGCATTTACGCTT 4132
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Qy 4133 TAGACGTAATTTGCAATTAAGTTTTCGACATGACCTTGAAGCGGACTGTTTCTAAGC 4192
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OY 4253 ACAGCCCCAGGAACCCCGCAAGTATGGGTACGATCAAGCCATTGCGCCGAATCTCCCGTA 4312
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OY 4313 GATTTCGGGTGTTCCAGCTAGCTGGGAAGGCAACAATTGATTTTGACAGCGGGAGAA 4372
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Db 3421 GATTTCGGGTGTTCCAGCTAGCTGGGAAGGCAACAATTGATTTTGACAGCGGGAGAA 3480
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Db 3481 CCAGAGTTATCTCTGACACAGCATAACTGTGTCGGGTGAACCCGAATCTTCTCAGCCT 3540
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Db 3601 AACACCACTGACTACTGTGTATCAGAGAAAAAATTGAAGCTCCCGTAAGAGATCG 3660
OY 4553 AATGGATCGCCCCGATTGGCATAGCCGGTGACATAAGACTACAACTGGCTTTCGGGT 4612
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OY 4673 ACCACTTTAGCAGTGCAGAAACCATGCGGACCTTAAAAACCCTTTCGGGTTCGGCCC 4732
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OY 4853 CAGATTGTGTCTCAAGCAATACAGAAATGTACTGATTTCCGACAACTAGACAAACAGCC 4912
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OY 5813 TCCACAGACTTGAAGCAATTAACGTCAAGAAAGTTACAGTATGCTCTCCACCCCCCTTC 5872
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OY 5873 CTAAACACAAAAATTAAAGATGTTCAAGAGTTCAAGTGCACGAAAGTACTGTTTAATC 5932
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QY 8333 GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCCGTATGAGGTAGACAATA 8392
Db 7441 GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCCGTATGAGGTAGACAATA 7500
QY 8393 TTACACCTGTCTACTGGCATTTAGAACTTTTGCCAGAGCAAAAGACATTCCAAAGCCA 8452
Db 7501 TTACACCTGTCTACTGGCATTTAGAACTTTTGCCAGAGCAAAAGACATTCCAAAGCCA 7560
QY 8453 TCAGAGGGGAATAAAGCATCTACGCGTGTCTTAATAGTCAGCATAGTACATTTTCAT 8512
Db 7561 TCAGAGGGGAATAAAGCATCTCTACGCGTGTCTTAATAGTCAGCATAGTACATTTTCAT 7620
QY 8513 CTGACTAATACTACAACACCAACCT 8539
Db 7621 CTGACTAATACTACAACACCAACCT 7647

RESULT 12
ABV73174
ID ABV73174 standard; DNA; 9951 BP.
XX
AC ABV73174;
XX
DT 08-JAN-2003 (first entry)
XX
DE Nucleotide sequence of Sinrep5 self replicating replicon.
XX
KM Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
KM hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; ds.
XX
OS Sindbis virus.
XX
PN WO200274920-A2.
XX
PD 26-SEP-2002.
XX
PF 18-MAR-2002; 2002WO-US008033.
XX
PR 16-MAR-2001; 2001US-0276854P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-740856/80.
XX
PT New nucleic acid molecule encoding an antigenic fusion polypeptide useful
PT as vaccines for enhancing or inducing immune responses, primarily
PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as
PT tumor or viral antigens.
XX
PS Disclosure; Page 56-58; 93pp; English.
XX
CC The invention relates to a nucleic acid molecule that encodes a fusion
CC polypeptide, comprising a first nucleic acid sequence encoding a
CC polypeptide that comprises at least one immunogenicity-potentiating
CC polypeptide, optionally, fused in frame with the nucleic acid, a linker
CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
CC in frame to them, and that encodes an antigenic peptide or polypeptide.
CC The nucleic acid molecule, polypeptides and vectors are useful as
CC vaccines for enhancing immune responses, primarily cytotoxic T
CC lymphocytes (CTL) responses to specific antigens such as tumour or viral
CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
CC The packaging cell line is useful for generating alphavirus replicon
CC particles without contamination from replicon-competent virus. The
CC pathogenic organisms include viruses such as human papilloma virus (HPV),
CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
CC as malaria, and bacteria that grow intracellularly such as mycobacteria
CC and listeria. The present sequence represents the nucleotide sequence of
CC the sindbis virus RNA replicon vector Sinrep5, a self replicating
CC replicon
XX
SQ Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;
Query Match 89.4%; Score 7637.4; DB 6; Length 9951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 121 AAAAAAGCTTCCCGCAATTGAGTAGACACAGAGTCACCTCCAATGACCATGCTA 180
QY 1073 ATGCCAGACATTTTCGATCTGGCCAGTAACATAATCGAGCTGAGGTTCTTACCACAG 1132
Db 181 ATGCCAGACATTTTCGATCTGGCCAGTAACATAATCGAGCTGAGGTTCTTACCACAG 240
QY 1133 CGACGATCTTGACATAGGCGACCGGCTCTGAGATGTTTCCGAGCACCATATC 1192
Db 241 CGACGATCTTGACATAGGCGACCGGCTCTGAGATGTTTCCGAGCACCATATC 300
QY 1193 ATTGTGTGCCCCATGCGTAGTCCAGAAAGCCCGGACCGCATGATGAATAACGCCAGTA 1252
Db 301 ATTGTGTGCCCCATGCGTAGTCCAGAAAGCCCGGACCGCATGATGAATAACGCCAGTA 360
QY 1253 AACTGGCGGAAAAACGTCGCAAGATTACAAACAGAACTTGCAATGAGAAATTAAAGATC 1312
Db 361 AACTGGCGGAAAAACGTCGCAAGATTACAAACAGAACTTGCAATGAGAAATTAAAGATC 420
QY 1313 TCCGACCGTACTTGATACGCCCGGATGCTGAACACCATCGCTCTGTTTCAACGATG 1372
Db 421 TCCGACCGTACTTGATACGCCCGGATGCTGAACACCATCGCTCTGTTTCAACGATG 480
QY 1373 TTACTGTCAACATGCGTCCGCAATATTCGTCATGCAAGACGTATATCAACGCTCCCG 1432
Db 481 TTACTGTCAACATGCGTCCGCAATATTCGTCATGCAAGACGTATATCAACGCTCCCG 540
QY 1433 GAACATATCTATCATCAGGCTATGAAGGCGTGCGGACCCCTGTACTGGATTGGCTTCGACA 1492
Db 541 GAACATATCTATCATCAGGCTATGAAGGCGTGCGGACCCCTGTACTGGATTGGCTTCGACA 600
QY 1493 CCACCAGTTTCATGTTCTCGGCTATGCGAGTTGTAACCTGCGTACAAACCACTGGG 1552
Db 601 CCACCAGTTTCATGTTCTCGGCTATGCGAGTTGTAACCTGCGTACAAACCACTGGG 660
QY 1553 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGACAAAGCTGAGTGAAG 1612
Db 661 CCGACGAGAAAGTCCTTGAAGCGCGTAACATCGGACTTTGCAGACAAAGCTGAGTGAAG 720
QY 1613 GTAGACAGGAAATTTGTCGATATGAGAGAAAGAGTTGAAGCCCGGTCGGGCTTT 1672
Db 721 GTAGACAGGAAATTTGTCGATATGAGAGAAAGAGTTGAAGCCCGGTCGGGCTTT 780
QY 1673 ATTTCTCCGTAGATGACACTTTATCCAGAACACAGAGCCAGCTTGACAGCTGGCATC 1732
Db 781 ATTTCTCCGTAGATGACACTTTATCCAGAACACAGAGCCAGCTTGACAGCTGGCATC 840
QY 1733 TTCCATCGGTGTTTCACTTGAATGGAAGCAGTGTACACTTGCCGCTGTGATACAGTGG 1792
Db 841 TTCCATCGGTGTTTCACTTGAATGGAAGCAGTGTACACTTGCCGCTGTGATACAGTGG 900
QY 1793 TGAAGTTCGAAAGGCTAGTAGTGAAGAAATCAACATCAGTCCCGGATCAGGGAGAAA 1852
Db 901 TGAAGTTCGAAAGGCTAGTAGTGAAGAAATCAACATCAGTCCCGGATCAGGGAGAAA 960
QY 1853 CCGTGGATACGCGGTTACACACAATAGCGAGGCTTCTGCTATGCAAAAGTTACTGACA 1912
Db 961 CCGTGGATACGCGGTTACACACAATAGCGAGGCTTCTGCTATGCAAAAGTTACTGACA 1020
QY 1913 CAGTAAAGGAGAAACGGGTATCGTTCCTGTGTGACGATACATCCCGGACCATATGCG 1972
Db 1021 CAGTAAAGGAGAAACGGGTATCGTTCCTGTGTGACGATACATCCCGGACCATATGCG 1080
QY 1973 ATCAGATGACTGTATATATGCGCACCGATATATCACTGACGATGACAAAACTTCTGG 2032
Db 1081 ATCAGATGACTGTATATATGCGCACCGATATATCACTGACGATGACAAAACTTCTGG 1140
QY 2033 TTGGGCTCAACCAAGCAATTTGTCATTAACGTTGAGACTTAACAGAAACCAACCATGTC 2092
Db 1141 TTGGGCTCAACCAAGCAATTTGTCATTAACGTTGAGACTTAACAGAAACCAACCATGTC 1200
QY 2093 AAATTACCTTCTGCGATCATAGACAAAGGTTCAAGCAATGGGCTAAGAGCGCAAGG 2152

Db 1201 AAAATTACCTTCTGCCGATCATAGCACAAAGGGTTCAGCAAAATGGGCTAAGGACCGCAAG 1260
QY 2153 ATGATCTTGATTAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 2212
Db 1261 ATGATCTTGATTAACGAGAAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGGCTGCT 1320
QY 2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTATCGCCCCACCTGGAACGACAGACT 2272
Db 1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTATCGCCCCACCTGGAACGACAGACT 1380
QY 2273 GCGTAAAAAGTCCAGACCTCTTTTAGCGCTTTCCCATGTCGTCCGTATGAGACGACTCTT 2332
Db 1381 GCGTAAAAAGTCCAGACCTCTTTTAGCGCTTTCCCATGTCGTCCGTATGAGACGACTCTT 1440
QY 2333 TGCCCATGTCGCTGAGGCGAAGAAATTGAAACTGGCATTTGCCAACCAAGAGAGAAAAAC 2392
Db 1441 TGCCCATGTCGCTGAGGCGAAGAAATTGAAACTGGCATTTGCCAACCAAGAGAGAAAAAC 1500
QY 2393 TGCTGCAAGTCTCGGAGGAATTAGTCATGAGGCCCAAGGCTGCTTTGAAGATGCTCAGG 2452
Db 1501 TGCTGCAAGTCTCGGAGGAATTAGTCATGAGGCCCAAGGCTGCTTTGAAGATGCTCAGG 1560
QY 2453 AGGAAGCCAGACGCGAGAAAGCTCCGAGAAACACTCCACCATTAGTGGCAGACAAAGGCA 2512
Db 1561 AGGAAGCCAGACGCGAGAAAGCTCCGAGAAACACTCCACCATTAGTGGCAGACAAAGGCA 1620
QY 2513 TCGAGGCGACGCGAGAAAGTGTCTGCGAAGTGAAGGGGCTCCAGCGGACATCGAGCAG 2572
Db 1621 TCGAGGCGACGCGAGAAAGTGTCTGCGAAGTGAAGGGGCTCCAGCGGACATCGAGCAG 1680
QY 2573 CATTAGTTGAAACCCCGCGGTCAAGTAAGATAATACCTCAAGCAAAATGACCGTATGA 2632
Db 1681 CATTAGTTGAAACCCCGCGGTCAAGTAAGATAATACCTCAAGCAAAATGACCGTATGA 1740
QY 2633 TCGGACAGTATTCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAACTCGCACCAG 2692
Db 1741 TCGGACAGTATTCGTTGTCTCGCCAAACTCTGTGCTGAAGAATGCCAACTCGCACCAG 1800
QY 2693 CGCACCCGCTAGCAGATCAGGTTAAGATCAATAACACACTCCGGAAGATCAGGAAGGTACG 2752
Db 1801 CGCACCCGCTAGCAGATCAGGTTAAGATCAATAACACACTCCGGAAGATCAGGAAGGTACG 1860
QY 2753 CGGTGAAACCATACGACGCTAAAGTACTGATGCCAGCAGAGAGGTGCCGTACCATGGCCAG 2812
Db 1861 CGGTGAAACCATACGACGCTAAAGTACTGATGCCAGCAGAGAGGTGCCGTACCATGGCCAG 1920
QY 2813 AATTCTTAGCATGAGTGAGAGCGCCACGTTAGTGTACCAAGAAAGAGATTGTGAACC 2872
Db 1921 AATTCTTAGCATGAGTGAGAGCGCCACGTTAGTGTACCAAGAAAGAGATTGTGAACC 1980
QY 2873 GCAAACTATACCACATTTGCCATGATGCGCCCGCAAGAATACAGAGAGAGCAGTACA 2932
Db 1981 GCAAACTATACCACATTTGCCATGATGCGCCCGCAAGAATACAGAGAGAGCAGTACA 2040
QY 2933 AGGTTACAAAGCAGAGCTTGCAAAACAGAGTACGTTTGAAGTGAACAAGAGCGTT 2992
Db 2041 AGGTTACAAAGCAGAGCTTGCAAAACAGAGTACGTTTGAAGTGAACAAGAGCGTT 2100
QY 2993 GCGTTAAGAAAGAAAGACCTCAGGTCGTCTCTCGGGAGAACTGACCAACCTCCCT 3052
Db 2101 GCGTTAAGAAAGAAAGACCTCAGGTCGTCTCTCGGGAGAACTGACCAACCTCCCT 2160
QY 3053 ATCATGAGTACGCTCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTAACAAGTGA 3112
Db 2161 ATCATGAGTACGCTCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTAACAAGTGA 2220
QY 3113 CAATAGAGTATAGGCACACCGGGGTGCGGCAAGTCAAGTATATCAAGTCAACTGTCA 3172
Db 2221 CAATAGAGTATAGGCACACCGGGGTGCGGCAAGTCAAGTATATCAAGTCAACTGTCA 2280
QY 3173 CGGCACGAGATCTTGTACCAGCGGAAAGAAAGAAATTTGCGGAAATTGAGCGCAGC 3232
Db 2281 CGGCACGAGATCTTGTACCAGCGGAAAGAAAGAAATTTGCGGAAATTGAGCGCAGC 2340

QY 3233 TGCTAAGACTGAGGGTATGCAGATTAACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 3292
Db 2341 TGCTAAGACTGAGGGTATGCAGATTAACGTCGAAGACAGTAGATTCGGTTATGCTCAACG 2400
QY 3293 GATGCCACAAAGCCGTAGAAAGTCTGTACGTTGACGGAAGCGTTCCGTCGCAAGCAGAGAG 3352
Db 2401 GATGCCACAAAGCCGTAGAAAGTCTGTACGTTGACGGAAGCGTTCCGTCGCAAGCAGAGAG 2460
QY 3353 CACTACTTGCTTGAATGCTATGCTCAGGCCCCGCAAGAAAGTACTATGCGGAGACC 3412
Db 2461 CACTACTTGCTTGAATGCTATGCTCAGGCCCCGCAAGAAAGTACTATGCGGAGACC 2520
QY 3413 CCATGCAATGCGGATTCCTTCAACATGATGCAACTAAAGTACATTTCAATCACCCGTAAA 3472
Db 2521 CCATGCAATGCGGATTCCTTCAACATGATGCAACTAAAGTACATTTCAATCACCCGTAAA 2580
QY 3473 AAGACATATGCACCAAGACATTTCTACAAGTATATCTCCGCGCTTGACACAGCCAGTTA 3532
Db 2581 AAGACATATGCACCAAGACATTTCTACAAGTATATCTCCGCGCTTGACACAGCCAGTTA 2640
QY 3533 CAGCTATTGTATGCACATGCAATTAAGATGAAAGATGAAACCAAGAACCCGTCGACAG 3592
Db 2641 CAGCTATTGTATGCACATGCAATTAAGATGAAAGATGAAACCAAGAACCCGTCGACAG 2700
QY 3593 AGAACATTGAATCGATATTTACAGGGGCCACAAAGCCGAAGGGGATATCATCTCTGA 3652
Db 2701 AGAACATTGAATCGATATTTACAGGGGCCACAAAGCCGAAGGGGATATCATCTCTGA 2760
QY 3653 CATGTTTCCGCGGGTGGTTAAGCAATTGCAAAATCGATATTCGCGACATGAAATGA 3712
Db 2761 CATGTTTCCGCGGGTGGTTAAGCAATTGCAAAATCGATATTCGCGACATGAAATGA 2820
QY 3713 CAGCGCGGCTCACAAGGGCTAACAGAAAAGAGTGTATGCCGTCCGCAAAAAGTCA 3772
Db 2821 CAGCGCGGCTCACAAGGGCTAACAGAAAAGAGTGTATGCCGTCCGCAAAAAGTCA 2880
QY 3773 ATGAAAACCCACTGTACGCGATCAATCAGAGCATGTGAAGTGTGCTCACCCGCACTG 3832
Db 2881 ATGAAAACCCACTGTACGCGATCAATCAGAGCATGTGAAGTGTGCTCACCCGCACTG 2940
QY 3833 AGGACAGGCTAGTGTGA AAACTTGACAGGGCGACCCGATTAAGCAGCCCACTAAC 3892
Db 2941 AGGACAGGCTAGTGTGA AAACTTGACAGGGCGACCCGATTAAGCAGCCCACTAAC 3000
QY 3893 TACCTAAAGAACTTTACAGGCTACTATAGAGACTGGGAAGCTGAACACAAAGGAATAA 3952
Db 3001 TACCTAAAGAACTTTACAGGCTACTATAGAGACTGGGAAGCTGAACACAAAGGAATAA 3060
QY 3953 TTGCTCAATTAACAGCCCCCACTCCCCGTGCCAATCCGTTCAAGTCAAGAACCAACGTTT 4012
Db 3061 TTGCTCAATTAACAGCCCCCACTCCCCGTGCCAATCCGTTCAAGTCAAGAACCAACGTTT 3120
QY 4013 GCTGGCGGAAAGCAATTGGAACCGATACTAGCCACGCGCGTATCTTACCGGTTGCC 4072
Db 3121 GCTGGCGGAAAGCAATTGGAACCGATACTAGCCACGCGCGTATCTTACCGGTTGCC 3180
QY 4073 AGTGAAGCGAAGTGTCCCAAGTTTGCAGATGACAAACCAATTCGGCCATTACGCTT 4132
Db 3181 AGTGAAGCGAAGTGTCCCAAGTTTGCAGATGACAAACCAATTCGGCCATTACGCTT 3240
QY 4133 TAGACGTAATTTGCATTAAGTTTTTCGGCATGCACTTGAACGCGGACTGTTTCTAAAC 4192
Db 3241 TAGACGTAATTTGCATTAAGTTTTTCGGCATGCACTTGAACGCGGACTGTTTCTAAAC 3300
QY 4193 AGACATCCCACTAACGTAACATCCCGCGATTCAGCGAGCCGCTAGCTCATTTGGGACA 4252
Db 3301 AGACATCCCACTAACGTAACATCCCGCGATTCAGCGAGCCGCTAGCTCATTTGGGACA 3360
QY 4253 ACAGCCCAAGAACCCGCAAGTATGGGTACGATCAGGCCATTGCCGCAACTCTCCGCTA 4312
Db 3361 ACAGCCCAAGAACCCGCAAGTATGGGTACGATCAGGCCATTGCCGCAACTCTCCGCTA 3420

QY	4313	GATTTCCGGTGTTCACGTAAGGGAAGGGCACACAACCTGATTGTCAGACGGGGAGA	4372
Db	3421	GATTTCCGGTGTTCACGTAAGGGAAGGGCACACAACCTGATTGTCAGACGGGGAGA	3480
QY	4373	CCAGAGTTATCTCTGCACAGCAATAACCTGGTCCCGGTGAACCGCAATCTTCTCAGCCT	4432
Db	3481	CCAGAGTTATCTCTGCACAGCAATAACCTGGTCCCGGTGAACCGCAATCTTCTCAGCCT	3540
QY	4433	TAGTCCCCGAGTACAGAGAGAACACCCGGCCCGGTCAAAAAATTCTTGAACCAAGTTCA	4492
Db	3541	TAGTCCCCGAGTACAGAGAGAACACCCGGCCCGGTCAAAAAATTCTTGAACCAAGTTCA	3600
QY	4493	AACACCACTCAGTACTTGTGTGATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAAATCG	4552
Db	3601	AACACCACTCAGTACTTGTGTGATCAGAGGAAAAAATTGAAGCTCCCCGTAAGAGAAATCG	3660
QY	4553	AATGATCGCCCCGATTGGCATAGCCGGTGAGATAAGAACTACAACCTGGCTTTCCGGT	4612
Db	3661	AATGATCGCCCCGATTGGCATAGCCGGTGAGATAAGAACTACAACCTGGCTTTCCGGT	3720
QY	4613	TTCCGCCGCGAGCAGCGGTACGACCTGGTTCATCAACATTTGGAATAATACAGAAACC	4672
Db	3721	TTCCGCCGCGAGCAGCGGTACGACCTGGTTCATCAACATTTGGAATAATACAGAAACC	3780
QY	4673	ACCACCTTCAGCAGTGCAGAACCATGCGCGACCTTAATAAACCTTTGCGTTCCGCC	4732
Db	3781	ACCACCTTCAGCAGTGCAGAACCATGCGCGACCTTAATAAACCTTTGCGTTCCGCC	3840
QY	4733	TGAATTGTTTAACTCAGAGGCAACCTCGTGTGAAGTCCATGGCTACGCCGACGCA	4792
Db	3841	TGAATTGCTTAACCCAGAGGCAACCTCGTGTGAAGTCCATGGCTACGCCGACGCA	3900
QY	4793	ACAGTGAGGACGTAGTCAACCGCTCTTGCCAGAAAGTTGTCAAGGTCTGACGCGAGAC	4852
Db	3901	ACAGTGAGGACGTAGTCAACCGCTCTTGCCAGAAAGTTGTCAAGGTCTGACGCGAGAC	3960
QY	4853	CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTCCGACAACCTAGACAACAGCC	4912
Db	3961	CAGATTGTGTCTCAAGCAATACAGAAATGTACCTGATTTCCGACAACCTAGACAACAGCC	4020
QY	4913	GTACACGGCAATTCACCCCGCAACATCTGAATTGCGTGAATTCGTCGGTATAGAGGTA	4972
Db	4021	GTACACGGCAATTCACCCCGCAACATCTGAATTGCGTGAATTCGTCGGTATAGAGGTA	4080
QY	4973	CAAGAGATGAGTTGGAGCCCGCGCTCATACCGCACCAAAAGGAGAATATTGCTGACT	5032
Db	4081	CAAGAGATGAGTTGGAGCCCGCGCTCATACCGCACCAAAAGGAGAATATTGCTGACT	4140
QY	5033	GTCAAGAGGAAGCAGTTGTCAACGACGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT	5092
Db	4141	GTCAAGAGGAAGCAGTTGTCAACGACGCCAATCCGCTGGGTAGACCAGGCGAAGGAGTCT	4200
QY	5093	GCCGTGCCATCTATAACGTTGGCCGACCAAGTTTACCGAATTCAGCCACGAGACAGGCA	5152
Db	4201	GCCGTGCCATCTATAACGTTGGCCGACCAAGTTTACCGAATTCAGCCACGAGACAGGCA	4260
QY	5153	CCGCAAGAATGACTGTGTGCTTAGGAAAAGAGTGAATCCAACGGGTCCGGCCCTGATTTCC	5212
Db	4261	CCGCAAGAATGACTGTGTGCTTAGGAAAAGAGTGAATCCAACGGGTCCGGCCCTGATTTCC	4320
QY	5213	GGAGACACCCAGAAAGCAGAAAGCTTGAATTTGCTACAAAAAGCCTACCATGACGTGGAG	5272
Db	4321	GGAGACACCCAGAAAGCAGAAAGCTTGAATTTGCTACAAAAAGCCTACCATGACGTGGAG	4380
QY	5273	ACTTAGTAATGAACATAAACATCAAGTCTGTGCGCAATTCGACTATCTACAGGCATTT	5332
Db	4381	ACTTAGTAATGAACATAAACATCAAGTCTGTGCGCAATTCGACTATCTACAGGCATTT	4440
QY	5333	ACGCAGCCGGAAAAAGACCGCCTTGAAGTATCACTTAAGTCTTGACAACCGCGCTAGACA	5392
Db	4441	ACGCAGCCGGAAAAAGACCGCCTTGAAGTATCACTTAAGTCTTGACAACCGCGCTAGACA	4500
QY	5393	GAACGTACCGCGGACGTAAACCTATTGCTCGATAGAAAGTGAAGGAAAGAAATGCACG	5452

Db	4501	GAACGTACGCGGACGTAAACCATCTATTGGCCCTGGATAGAGAAGTGGAGGAAAGAAATCGACG	4560
Qy	5453	CGGCACCTCCAACTTAAGAGTCTGTAAACAGAGCTGAAGATGAAGATATGGAGATCGACG	5512
Db	4561	CGGCACTCCAACTTAAGGAGTCTGTAAACAGAGCTGAAGATGAAGATATGGAGATCGACG	4620
Qy	5513	ATGAGTTAGTATGGATTCACTCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTA	5572
Db	4621	ATGAGTTAGTATGGATTCACTCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTA	4680
Qy	5573	CAAAAGGAAAATGTATTTCGTACTTCGAAGGCAACCAATTCATCAAGCAGCAAAAGACA	5632
Db	4681	CAAAAGGAAAATGTATTTCGTACTTCGAAGGCAACCAATTCATCAAGCAGCAAAAGACA	4740
Qy	5633	TGGCGAGATAAAGGTCCTGTTCCTTAATGACCAGGAAAATATGAACAACCTGTGTGCT	5692
Db	4741	TGGCGAGATAAAGGTCCTGTTCCTTAATGACCAGGAAAATATGAACAACCTGTGTGCT	4800
Qy	5693	ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGTGCACCAATACCCGT	5752
Db	4801	ACATATTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTGCCCGTGCACCAATACCCGT	4860
Qy	5753	CGTCTAGCCCGCCCAAAACGTTGCCGTGCTTGCATGTATGCCATGACGCGAAGAGG	5812
Db	4861	CGTCTAGCCCGCCCAAAACGTTGCCGTGCTTGCATGTATGCCATGACGCGAAGAGG	4920
Qy	5813	TCCACAGACTTGAAGCAATACGTCAAGAAAGTTACAGTATGCTCCTCCACCCCTTC	5872
Db	4921	TCCACAGACTTGAAGCAATACGTCAAGAAAGTTACAGTATGCTCCTCCACCCCTTC	4980
Qy	5873	CTAAGCACAAATTAAGAAATGTTCAAGAGTTCAAGTGCACGAAAGTAGTCTGTATTATC	5932
Db	4981	CTAAGCACAAATTAAGAAATGTTCAAGAGTTCAAGTGCACGAAAGTAGTCTGTATTATC	5040
Qy	5933	CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTCCAGAACGCTTACCG	5992
Db	5041	CGCACACTCCCGCATTCGTTCCCGCCCGTAAGTACATAGAAGTCCAGAACGCTTACCG	5100
Qy	5993	CTCCTCCTGCACAGGCCGAGAGGCCCCCGAAAGTTGAGCCACACCGTCACTTACAG	6052
Db	5101	CTCCTCCTGCACAGGCCGAGAGGCCCCCGAAAGTTGAGCCACACCGTCACTTACAG	5160
Qy	6053	CTGATTAACACTCGCTTGATGTCAAGACATCTCACTGGATATGATGACAGTAGCGAAG	6112
Db	5161	CTGATTAACACTCGCTTGATGTCAAGACATCTCACTGGATATGATGACAGTAGCGAAG	5220
Qy	6113	GCTCACTTTTTCGAGCTTTAGCGGATCGGACAACCTCTATTACTAGTATGACAGTTGGT	6172
Db	5221	GCTCACTTTTTCGAGCTTTAGCGGATCGGACAACCTCTATTACTAGTATGACAGTTGGT	5280
Qy	6173	CGTCAGGACCTAGTTCACCTAGAGATAGTAGACCGAAGCAGGTGGTGGCTGACGTTTC	6232
Db	5281	CGTCAGGACCTAGTTCACCTAGAGATAGTAGACCGAAGCAGGTGGTGGCTGACGTTTC	5340
Qy	6233	ATGCCGTCCAAAGAGCCTGCCCTTAATTCCACCGCCAAAGCTTAAAGAGATGCCCGCTGG	6292
Db	5341	ATGCCGTCCAAAGAGCCTGCCCTTAATTCCACCGCCAAAGCTTAAAGAGATGCCCGCTGG	5400
Qy	6293	CAGCGGCAAGAAAAGAGCCCACTCCACCGCAAGCAATAGCTCTGAGTCCCTCCACCTCT	6352
Db	5401	CAGCGGCAAGAAAAGAGCCCACTCCACCGCAAGCAATAGCTCTGAGTCCCTCCACCTCT	5460
Qy	6353	CTTTTGGTGGGTATCCATGTCCCTCGGATCAATTTTGAACGAGAGACGGCCCCGACAGG	6412
Db	5461	CTTTTGGTGGGTATCCATGTCCCTCGGATCAATTTTGAACGAGAGACGGCCCCGACAGG	5520
Qy	6413	CAGCGGTACAAACCCCTGGCAACAGGCCCCACCGAGATGCTATGTCTTTCGATCGTTT	6472
Db	5521	CAGCGGTACAAACCCCTGGCAACAGGCCCCACCGAGATGCTATGTCTTTCGATCGTTT	5580
Qy	6473	CCGACGAGAGATTGATGAGCTGACCGCAGAGTAACTGAGTCCGAACCGGTCTGTTTG	6532

Db 5581 CCGACGAGAGATTGATGAGCTGAGCCGACAGAGTAAGTCCGAACCCGTCCTGTTG 5640
 QY 6533 GATCATTTTGAACCGGGCGAAGTGAATCAATTATATCGTCCCGATCAGCCGATCTTTTC 6592
 Db 5641 GATCATTTTGAACCGGGCGAAGTGAATCAATTATATCGTCCCGATCAGCCGATCTTTTC 5700
 QY 6593 CACTACGCAAGCAGAGACGTAGACGAGGAGCAGAGGAGTGAATTAAGTAAACCGGGG 6652
 Db 5701 CACTACGCAAGCAGAGACGTAGACGAGGAGCAGAGGAGTGAATTAAGTAAACCGGGG 5760
 QY 6653 TAGGTGGGTACATATTTTCGACGGAACAAGCCCTGGGCACTTGCAAAAAGAGTCCGTTTC 6712
 Db 5761 TAGGTGGGTACATATTTTCGACGGAACAAGCCCTGGGCACTTGCAAAAAGAGTCCGTTTC 5820
 QY 6713 TGCAGAACGAGCTTACAGAACCGACCTTGAGCGCAATGTCTTGAAAGAAATTCATGCCCC 6772
 Db 5821 TGCAGAACGAGCTTACAGAACCGACCTTGAGCGCAATGTCTTGAAAGAAATTCATGCCCC 5880
 QY 6773 CGGTGCTCGACACGTCGAAAGAGAACAACTCAACTCAGGTACAGATGATGCCCAACG 6832
 Db 5881 CGGTGCTCGACACGTCGAAAGAGAACAACTCAACTCAGGTACAGATGATGCCCAACG 5940
 QY 6833 AAGCCAAACAAAGTAGTACGACCTGCTGTAAGTAGAAATCAGAAAGCCATAACCACTG 6892
 Db 5941 AAGCCAAACAAAGTAGTACGACCTGCTGTAAGTAGAAATCAGAAAGCCATAACCACTG 6000
 QY 6893 AGCGACTACTGTACGACCTGCTGTAAGTAGAAATCAGAAAGCCATAACCACTG 6952
 Db 6001 AGCGACTACTGTACGACCTGCTGTAAGTAGAAATCAGAAAGCCATAACCACTG 6060
 QY 6953 AGATCACTATCCGAAACCATTTGACTCCAGTAGCGTACCGCGCACTACTCCGATCCAC 7012
 Db 6061 AGATCACTATCCGAAACCATTTGACTCCAGTAGCGTACCGCGCACTACTCCGATCCAC 6120
 QY 7013 AGTTCGCTGAGCTGTCTGTACCACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 7072
 Db 6121 AGTTCGCTGAGCTGTCTGTACCACTATCTGCATGAGAACTATCCGACAGTAGCATCTT 6180
 QY 7073 ATCAGATTAATGACGAGTACGATGCTTAATTTGGATATGTTAGACGAGACAGTCCGATGCC 7132
 Db 6181 ATCAGATTAATGACGAGTACGATGCTTAATTTGGATATGTTAGACGAGACAGTCCGATGCC 6240
 QY 7133 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATA 7192
 Db 6241 TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAACATGAGTATA 6300
 QY 7193 GAGCCCCGAATATCCGAGTGCCTTCATCAGCGATGACGAGACGCTACAAATATGTC 7252
 Db 6301 GAGCCCCGAATATCCGAGTGCCTTCATCAGCGATGACGAGACGCTACAAATATGTC 6360
 QY 7253 TCATTGCCGCACTAAAGAAATTGCAAGTCAAGCAGATGCGTGAACCTGCCAACACTGG 7312
 Db 6361 TCATTGCCGCACTAAAGAAATTGCAAGTCAAGCAGATGCGTGAACCTGCCAACACTGG 6420
 QY 7313 ACTCAGCGCATTTCAATGTGCAATGCTTTGCAAAATATGCAATGTAATGACGAGTATGGG 7372
 Db 6421 ACTCAGCGCATTTCAATGTGCAATGCTTTGCAAAATATGCAATGTAATGACGAGTATGGG 6480
 QY 7373 AGGAGTTCGCTCGGAAGCCAAATTAGATTAACAAGTTGTCACCGCATATGTAGCTA 7432
 Db 6481 AGGAGTTCGCTCGGAAGCCAAATTAGATTAACAAGTTGTCACCGCATATGTAGCTA 6540
 QY 7433 GACTGAAAGGCCCTAAGGCCGCGCACTATTTGCAAAAGACGTATAATTGGTCCCATGGC 7492
 Db 6541 GACTGAAAGGCCCTAAGGCCGCGCACTATTTGCAAAAGACGTATAATTGGTCCCATGGC 6600
 QY 7493 AAGAAGTGCCTATGATAGATTGCTCATGACATGAAAAGAGACGTGAAGTTACACCAAG 7552
 Db 6601 AAGAAGTGCCTATGATAGATTGCTCATGACATGAAAAGAGACGTGAAGTTACACCAAG 6660
 QY 7553 GCACGAAACACACAGAAAGAAAGACCGAAAGTACAAAGTATCAAGCCGACGAAACCCCTGG 7612
 Db 6661 GCACGAAACACACAGAAAGAAAGACCGAAAGTATCAAGTATCAAGCCGACGAAACCCCTGG 6720

QY 7613 CGACTGCTTACTTATGCGGGAATTCACCCGGGAATTAAGTCCGTAGGCTTACGGCCGCTTTCG 7672
 Db 6721 CGACTGCTTACTTATGCGGGAATTCACCCGGGAATTAAGTCCGTAGGCTTACGGCCGCTTTCG 6780
 QY 7673 TTCCAAACATTCACACGCTTTTGAACATGTCGCGGAGGATTTTGAATGCAATCATAGCAG 7732
 Db 6781 TTCCAAACATTCACACGCTTTTGAACATGTCGCGGAGGATTTTGAATGCAATCATAGCAG 6840
 QY 7733 AACACTTCAAGCAAGCGCACCCGGTACTGAGACGGAATTCGCATCATTTGCACAAAAGCC 7792
 Db 6841 AACACTTCAAGCAAGCGCACCCGGTACTGAGACGGAATTCGCATCATTTGCACAAAAGCC 6900
 QY 7793 AAGACGACGCTATGCGCTTAACCGGTCTGATGATCTTGAGAGAACCTGGGTGTGATCAAC 7852
 Db 6901 AAGACGACGCTATGCGCTTAACCGGTCTGATGATCTTGAGAGAACCTGGGTGTGATCAAC 6960
 QY 7853 CACTACTCGACTTGATCGAGTGCCTTTGAGAAATATCATCCACCATCTACCTACGG 7912
 Db 6961 CACTACTCGACTTGATCGAGTGCCTTTGAGAAATATCATCCACCATCTACCTACGG 7020
 QY 7913 GTACTCGTTTAAATTCGGGCGATGATGAATCCGGAATGTTCTCACACTTTTGTCA 7972
 Db 7021 GTACTCGTTTAAATTCGGGCGATGATGAATCCGGAATGTTCTCACACTTTTGTCA 7080
 QY 7973 ACACAGTTTGAATGTCGTTATCCGACAGAGTACTGAAGACGGCTTAAACGTCGA 8032
 Db 7081 ACACAGTTTGAATGTCGTTATCCGACAGAGTACTGAAGACGGCTTAAACGTCGA 7140
 QY 8033 GATGTGCAAGCGTTCAATGGCGACGACAAATCATATCATGAGTAGTATCTGACAAAGAA 8092
 Db 7141 GATGTGCAAGCGTTCAATGGCGACGACAAATCATATCATGAGTAGTATCTGACAAAGAA 7200
 QY 8093 TGGGTGAGAGGTGCGCCACCTGGCTCAACATGAGGTTAAGTATCATGACGAGTCAATCG 8152
 Db 7201 TGGGTGAGAGGTGCGCCACCTGGCTCAACATGAGGTTAAGTATCATGACGAGTCAATCG 7260
 QY 8153 GTGAGAGACCACTTACTTCTGCGCGGAGTTATCTTGCAAGATTGCGTTACTTCCACAG 8212
 Db 7261 GTGAGAGACCACTTACTTCTGCGCGGAGTTATCTTGCAAGATTGCGTTACTTCCACAG 7320
 QY 8213 CGTGCCGCTGCGGATCCCTGAAAGGCTGTTAAGTTGGGTAAACCGCTCCCAAGCCG 8272
 Db 7321 CGTGCCGCTGCGGATCCCTGAAAGGCTGTTAAGTTGGGTAAACCGCTCCCAAGCCG 7380
 QY 8273 ACACGAGCAAGACGAGACGAGACGCGCTCTGCTAGATGAACAAGGCGTGTGTTA 8332
 Db 7381 ACACGAGCAAGACGAGACGAGACGCGCTCTGCTAGATGAACAAGGCGTGTGTTA 7440
 QY 8333 GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCCGTATGAGGTAGACAATA 8392
 Db 7441 GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCCGTATGAGGTAGACAATA 7500
 QY 8393 TTACACTGTCTTACTGCGATGAGAACTTTGCCCAGAGCAAAAGACATTCCAAGCCA 8452
 Db 7501 TTACACTGTCTTACTGCGATGAGAACTTTGCCCAGAGCAAAAGACATTCCAAGCCA 7560
 QY 8453 TCAGAGGGGAAATTAAGCATCTCTACGGTGTCTTAAATAGTCAGCATAGTACATTTCAAT 8512
 Db 7561 TCAGAGGGGAAATTAAGCATCTCTACGGTGTCTTAAATAGTCAGCATAGTACATTTCAAT 7620
 QY 8513 CTGACTAATACTACACACCAACCT 8539
 Db 7621 CTGACTAATACTACACACCAACCT 7647

RESULT 13
 ABN86689 standard; DNA; 12110 BP.
 ID ABN86689
 AC ABN86689;
 XX
 DT 05-NOV-2002 (first entry)

XX Nucleotide sequence of vector Sinrep5-E7-Hsp70.
DE
XX Major histocompatibility complex; MHC; antigen presenting cell; APC;
KM antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic;
KW cancer; viral infection; HPV; E7; heat shock protein 70; Hsp70; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 7715..9819
FT /tag= a
FT /note= "E7-Hsp70 fusion sequence"
XX
PN WO200261113-A2.
XX
PD 08-AUG-2002.
XX
PF 01-FEB-2002; 2002WO-US002598.
XX
PR 01-FEB-2001; 2001US-0265334P.
XX
PA (UWJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-619261/66.
XX
XX Nucleic acid molecule encoding a fusion polypeptide that promotes
PT processing via the Major Histocompatibility Complex class I pathway
PT and/or promotes activity of an antigen presenting cell, useful as vaccine
PT for cancer and viral infections.
XX
PS Claim 36; Page 30-33; 127pp; English.
XX
XX The invention relates to a new nucleic acid molecule (I) encoding a
CC fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC nucleic acid sequence encoding a first polypeptide or peptide that
CC promotes processing via the Major Histocompatibility Complex (MHC) class
CC I pathway (MHC-I-PP) and/or promotes development or activity of an
CC antigen presenting cell (APC). The second nucleic acid sequence is linked
CC in frame to the first nucleic acid sequence or to a linker nucleic acid
CC sequence and encodes an antigenic polypeptide or peptide. The methods and
CC compositions of the present invention are useful as therapeutic vaccine
CC for cancer and for major viral infections, such as hepatoma and cervical
CC cancer, that cause morbidity and mortality. They can also be used in
CC treating animal diseases, such as equine herpesvirus, bovine viruses,
CC Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC veterinary medicine context. The present sequence represents the
CC nucleotide sequence of vector Sinrep5-E7-Hsp70 comprising the human
CC papillomavirus (HPV) E7 antigenic protein and M. tuberculosis heat shock
CC protein 70 (Hsp70) fusion sequence
XX
SQ Sequence 12110 BP; 3339 A; 3084 C; 3137 G; 2550 T; 0 U; 0 Other;
Query Match 89.4%; Score 7637.4; DB 6; Length 12110;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 893 ATTGACGGCGTAGTACACACTATTGAATCAACAGCCGCAATTGCATCACTACACAA 952
DB 1 ATTGACGGCGTAGTACACACTATTGAATCAACAGCCGCAATTGCATCACTACACAA 60
QY 953 TGGAGAAGCCAGTAGTAACGTAGACGTAGACCCCGAGAGTCCGTTGTCGTGCAACTGC 1012
DB 61 TGGAGAAGCCAGTAGTAACGTAGACGTAGACCCCGAGAGTCCGTTGTCGTGCAACTGC 120
QY 1013 AAAAAGCTTCCCGCAATTGAGGTAGTACACAGAGTCACTCCAAATGACCATGCTA 1072
DB 121 AAAAAGCTTCCCGCAATTGAGGTAGTACACAGAGTCACTCCAAATGACCATGCTA 180
QY 1073 ATGCCAGAGCATTTTCGATCTGGCCAGTAACATAATCGAGCTGGAGGTTCTTACCACAG 1132

DB 181 ATGCCAGAGCATTTTCGATCTGGCCAGTAACATAATCGAGCTGAGGTTCTTACCACAG 240
QY 1133 CGACGATCTTGACATAGGACGCCGACCGGCTCGTAGAATGTTTTCCGACCAACAGTATC 1192
DB 241 CGACGATCTTGACATAGGACGCCGACCGGCTCGTAGAATGTTTTCCGACCAACAGTATC 300
QY 1193 ATTGTGTCGCCCATGCGTAGTCCAGAAAGCCCGGACCGCATGATGAATAACGCCAGTA 1252
DB 301 ATTGTGTCGCCCATGCGTAGTCCAGAAAGCCCGGACCGCATGATGAATAACGCCAGTA 360
QY 1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAATTAAGGATC 1312
DB 361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGCATGAGAAATTAAGGATC 420
QY 1313 TCCGACCGTACTGTATACGCCCGGATGCTGAACACCATCGCTCTGCTTCAACAGATG 1372
DB 421 TCCGACCGTACTGTATACGCCCGGATGCTGAACACCATCGCTCTGCTTCAACAGATG 480
QY 1373 TTACCTGCACATGCGTCCGCAATATTCGTCATGCAAGAGCGTGTATATCAACGCTCCCG 1432
DB 481 TTACCTGCACATGCGTCCGCAATATTCGTCATGCAAGAGCGTGTATATCAACGCTCCCG 540
QY 1433 GAACATATCTATCATCAGGCTATGAAGGCGTGCGGACCCCTGTACTGGAATTGGCTTGACA 1492
DB 541 GAACATATCTATCATCAGGCTATGAAGGCGTGCGGACCCCTGTACTGGAATTGGCTTGACA 600
QY 1493 CCACCCAGTTCAATGTTCTCGGCTATGCGAGTTCGTAACCCCTGCGTCAACCAACTGGG 1552
DB 601 CCACCCAGTTCAATGTTCTCGGCTATGCGAGTTCGTAACCCCTGCGTCAACCAACTGGG 660
QY 1553 CCGACGAGAAAGTCTTGAAGCGCGTAACTCGGACTTTGCAGACAAAGCTGAGTGAAG 1612
DB 661 CCGACGAGAAAGTCTTGAAGCGCGTAACTCGGACTTTGCAGACAAAGCTGAGTGAAG 720
QY 1613 GTAGGACAGGAAAAATTGTCGATATAGAGGAAGAGGATTGAAGCCCGGCTCGCGGTTT 1672
DB 721 GTAGGACAGGAAAAATTGTCGATATAGAGGAAGAGGATTGAAGCCCGGCTCGCGGTTT 780
QY 1673 ATTTCTCCGTAGGATCGACACTTTATCCAGAAACAGAGCCAGCTTGAGAGCTGGCATC 1732
DB 781 ATTTCTCCGTAGGATCGACACTTTATCCAGAAACAGAGCCAGCTTGAGAGCTGGCATC 840
QY 1733 TTCCATCGGTTTCCACTTGAATGAAAGAGTGTGTAACACTTGCCTGTGATACAGTGG 1792
DB 841 TTCCATCGGTTTCCACTTGAATGAAAGAGTGTGTAACACTTGCCTGTGATACAGTGG 900
QY 1793 TGAAGTCCGAAAGGCTACGTAGTGAAGAAATCAACCATCACTCCCGGATCAACGGGAGAAA 1852
DB 901 TGAAGTCCGAAAGGCTACGTAGTGAAGAAATCAACCATCACTCCCGGATCAACGGGAGAAA 960
QY 1853 CCGTGGGATACCGGTTACACACAATAGCGAGGCTTCTGTATGCAAGTTACTGACA 1912
DB 961 CCGTGGGATACCGGTTACACACAATAGCGAGGCTTCTGTATGCAAGTTACTGACA 1020
QY 1913 CAGTAAAGGAGAAAGGATATGCTGCTGTGTGACGTAACATCCCGGCAACCATATGCG 1972
DB 1021 CAGTAAAGGAGAAAGGATATGCTGCTGTGTGACGTAACATCCCGGCAACCATATGCG 1080
QY 1973 ATCAGATGACTGTATATATGCCCACGGATATATCACTGACGATGACAAAACTTCTGG 2032
DB 1081 ATCAGATGACTGTATATATGCCCACGGATATATCACTGACGATGACAAAACTTCTGG 1140
QY 2033 TTGGGCTCAACGACGGAATTGTCTATTAAACGTAAGACTAACAGGAACCAACCATGTC 2092
DB 1141 TTGGGCTCAACGACGGAATTGTCTATTAAACGTAAGACTAACAGGAACCAACCATGTC 1200
QY 2093 AAAATTACCTTCTGCGGATCATAGCACAAGGTTCAAGAAATGGGCTTAAGAGCGCAAG 2152
DB 1201 AAAATTACCTTCTGCGGATCATAGCACAAGGTTCAAGAAATGGGCTTAAGAGCGCAAG 1260
QY 2153 ATGATCTTGATTAACGAGAAATGCTGGTACTAGAGAACGCAAGCTTAAGCTATGGCTGCT 2212
DB 1261 ATGATCTTGATTAACGAGAAATGCTGGTACTAGAGAACGCAAGCTTAAGCTATGGCTGCT 1320

QY	2213	TGTGGCGGTTTCGCACTAAGAAAGTACATTCGTTTATTCGCCCACTTGAAACGACAGCTT	2272
Db	1321	TGTGGCGGTTTCGCACTAAGAAAGTACATTCGTTTATTCGCCCACTTGAAACGACAGCTT	1380
QY	2273	GCGTAAAGTCCCAAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGACGACCTCTT	2332
Db	1381	GCGTAAAGTCCCAAGCCTCTTTTAGCGCTTTTCCCATGTCGTCCGTATGACGACCTCTT	1440
QY	2333	TGCCCATGTCGCTGAGGCGAAGAAATTGAAACTGGCATTCGAACCAAGAAGAGAAAAAC	2392
Db	1441	TGCCCATGTCGCTGAGGCGAAGAAATTGAAACTGGCATTCGAACCAAGAAGAGAAAAAC	1500
QY	2393	TGCTGCAGGTCCTCGAGAGAAATTAGTCATGAGGCGCAAGGCTGCTTTTGAGGATGCTCAGG	2452
Db	1501	TGCTGCAGGTCCTCGAGAGAAATTAGTCATGAGGCGCAAGGCTGCTTTTGAGGATGCTCAGG	1560
QY	2453	AGGAAGCCAGAGCGGAGAACTCCGAGAAGCACTTCCACCATTAAGTGCGACAGCAAAGCA	2512
Db	1561	AGGAAGCCAGAGCGGAGAACTCCGAGAAGCACTTCCACCATTAAGTGCGACAGCAAAGCA	1620
QY	2513	TCGAGGCGAGCCGAGAAAGTTGTCGGAAGTGAAGGGGCTCCAGGCGACATCGAGCAG	2572
Db	1621	TCGAGGCGAGCCGAGAAAGTTGTCGGAAGTGAAGGGGCTCCAGGCGACATCGAGCAG	1680
QY	2573	CATTAGTTGAACCCCGCGCGTCAAGTAAGGATAATTAACCTCAAGCAATGACCCGTATGA	2632
Db	1681	CATTAGTTGAACCCCGCGCGTCAAGTAAGGATAATTAACCTCAAGCAATGACCCGTATGA	1740
QY	2633	TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAAATGCCAACTCGCACAG	2692
Db	1741	TCGGACAGTATATCGTTGTCTCGCCAAACTCTGTGCTGAAGAAATGCCAACTCGCACAG	1800
QY	2693	CGCACCCGCTAGCAGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGTTACG	2752
Db	1801	CGCACCCGCTAGCAGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGTTACG	1860
QY	2753	CGGTGGAACCATACGACGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAG	2812
Db	1861	CGGTGGAACCATACGACGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAG	1920
QY	2813	AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAAAGAAAGAGTTGTGAACC	2872
Db	1921	AATTCCTAGCACTGAGTGAGAGCGCCACGTTAGTGTACAAAGAAAGAGTTGTGAACC	1980
QY	2873	GCAAACTATACCAACATTGCCATGTCATGGCCCCGCCAAGATAAGAAAGAGCAGTACA	2932
Db	1981	GCAAACTATACCAACATTGCCATGTCATGGCCCCGCCAAGATAAGAAAGAGCAGTACA	2040
QY	2933	AGGTTACAAAGGCAAGCCTTGCAAGAAACAGAGTACGTTTGAAGTGACAAGAACGTT	2992
Db	2041	AGGTTACAAAGGCAAGCCTTGCAAGAAACAGAGTACGTTTGAAGTGACAAGAACGTT	2100
QY	2993	GCGTTAAGAAGAGAAGCCTCAGGTCGTCTCGGGAAGACTGACCAACCTCCCT	3052
Db	2101	GCGTTAAGAAGAGAAGCCTCAGGTCGTCTCGGGAAGACTGACCAACCTCCCT	2160
QY	3053	ATCATGAGCTAGCTCTGAGAGGAACTGAAGACCCGACCTGCGGTCGCCGTACAAGTTCGAAA	3112
Db	2161	ATCATGAGCTAGCTCTGAGAGGAACTGAAGACCCGACCTGCGGTCGCCGTACAAGTTCGAAA	2220
QY	3113	CAATAGAGTGAATAGGCAACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA	3172
Db	2221	CAATAGAGTGAATAGGCAACCGGGGTCGGGCAAGTCAGCTATTATCAAGTCAACTGTCA	2280
QY	3173	CGGCACGAGATCTTGTTCACGCGAAAGAAAGAAATTGTCGGAATTGAGGCCGACG	3232
Db	2281	CGGCACGAGATCTTGTTCACGCGAAAGAAAGAAATTGTCGGAATTGAGGCCGACG	2340
QY	3233	TGCTAAGACTGAGGGGTATGAGATTACGTCGAAGACAGTAGATTCCGTTATGCTCAACG	3292
Db	2341	TGCTAAGACTGAGGGGTATGAGATTACGTCGAAGACAGTAGATTCCGTTATGCTCAACG	2400

QY	3293	GATGCGCACAAAAGCCCGTAGAAGTGTCTGTACGTTTGAACGAAGCGTTCCGGTGCCACGCAAGAG	3352
Db	2401	GATGCGCACAAAAGCCCGTAGAAGTGTCTGTACGTTTGAACGAAGCGTTCCGGTGCCACGCAAGAG	2460
QY	3353	CACACTTGTCCCTTGATTGCTATCGTCAGGCCCCCGCAAGAGGTAGTACTATGCGGAGACC	3412
Db	2461	CACACTTGTCCCTTGATTGCTATCGTCAGGCCCCCGCAAGAGGTAGTACTATGCGGAGACC	2520
QY	3413	CCATGCAATGCGGATTCCTCAACATGATGCACTAAAGTACATTTCAATCACCCCTGAAA	3472
Db	2521	CCATGCAATGCGGATTCCTCAACATGATGCACTAAAGTACATTTCAATCACCCCTGAAA	2580
QY	3473	AAGACATATGCACCAAGA CATTTCTACAAGTATATCTCCCGCGTTGCA CACAGCCAGTTA	3532
Db	2581	AAGACATATGCACCAAGA CATTTCTACAAGTATATCTCCCGCGTTGCA CACAGCCAGTTA	2640
QY	3533	CAGCTATTGTATCGACACTGCACTTACGATGGAAAGATGAAAACCAACGACCCTGCAAGA	3592
Db	2641	CAGCTATTGTATCGACACTGCACTTACGATGGAAAGATGAAAACCAACGACCCTGCAAGA	2700
QY	3593	AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCTGA	3652
Db	2701	AGAACATTGAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCTGA	2760
QY	3653	CATGTTTCCGGGGGTGTTAAGCAATTGCAAAATCGACTATCCCGACATGAAGTAAATGA	3712
Db	2761	CATGTTTCCGGGGGTGTTAAGCAATTGCAAAATCGACTATCCCGACATGAAGTAAATGA	2820
QY	3713	CAGCGCGGCTCTACAAGGGCTTAACAGAAAAGAGTGTATGCGCTCCGGCAAAAAGTCA	3772
Db	2821	CAGCGCGGCTCTACAAGGGCTTAACAGAAAAGAGTGTATGCGCTCCGGCAAAAAGTCA	2880
QY	3773	ATGAAAACCCCACTGTACGCGATCACATCAGACGATGTGAACGTGTGCTCACCCGCACTG	3832
Db	2881	ATGAAAACCCCACTGTGTACGCGATCACATCAGACGATGTGAACGTGTGCTCACCCGCACTG	2940
QY	3833	AGGACAGGCTAGTGTGAAAACTTGCAAGGCGGACCCATGATTTAAGACGCCCACTAACA	3892
Db	2941	AGGACAGGCTAGTGTGAAAACTTGCAAGGCGGACCCATGATTTAAGACGCCCACTAACA	3000
QY	3893	TACCTAAAGGAACTTTCAAGGCTACTATAGAGGACTGGGAAGCTGAACA CAAGGGAATTA	3952
Db	3001	TACCTAAAGGAACTTTCAAGGCTACTATAGAGGACTGGGAAGCTGAACA CAAGGGAATTA	3060
QY	3953	TTGTGCAATTAACAGCCCCACTCCCCGTGCCAATCCGTTCACTGCAAGACCAACGTTT	4012
Db	3061	TTGTGCAATTAACAGCCCCACTCCCCGTGCCAATCCGTTCACTGCAAGACCAACGTTT	3120
QY	4013	GCTGGCGGAAAAGCATTGGAA CCGATACTAGCCACGGCCGATCGTACTTACCGGTTGCC	4072
Db	3121	GCTGGCGGAAAAGCATTGGAA CCGATACTAGCCACGGCCGATCGTACTTACCGGTTGCC	3180
QY	4073	AGTGAAGCGAAGCTGTTCCCA CAGTTTGGCGATGACAAACCACTTGGGCCATTTACGCCCT	4132
Db	3181	AGTGAAGCGAAGCTGTTCCCA CAGTTTGGCGATGACAAACCACTTGGGCCATTTACGCCCT	3240
QY	4133	TAGACGTAATTTGCAATTAAGTTTTTTCGGCATGGA CTTGACAAGCGGACTGTTTTCTAAAC	4192
Db	3241	TAGACGTAATTTGCAATTAAGTTTTTTCGGCATGGA CTTGACAAGCGGACTGTTTTCTAAAC	3300
QY	4193	AGAGCATCCCACTAACGTACCATCCCGCCGATTCA GCGAGGCGCGTAGCTCATTTGGGACA	4252
Db	3301	AGAGCATCCCACTAACGTACCATCCCGCCGATTCA GCGAGGCGCGTAGCTCATTTGGGACA	3360
QY	4253	ACAGCCCAAGAAACCCGCAAGTATGGTACGATCA CGCCATTGCGCGGAACTCTCCCGTA	4312
Db	3361	ACAGCCCAAGAAACCCGCAAGTATGGTACGATCA CGCCATTGCGCGGAACTCTCCCGTA	3420
QY	4313	GATTTCCGGTGTTCAGCTAGCTGGGAAGGSCACA CAACCTTGATTTGCAGACGGGAGAA	4372
Db	3421	GATTTCCGGTGTTCAGCTAGCTGGGAAGGSCACA CAACCTTGATTTGCAGACGGGAGAA	3480
QY	4373	CCAGAGTTATCTCTGCACAGCATTAACCTGGTCCCGGTGAACCGCAATCTTCTCACGCGCT	4432

Db 3481 CCAGAGTTATCTGACAGCATTAACCTGTCCTGGTAACCGCAATCTTCTCACGCCCT 3540
Qy 4433 TAGTCCCGAGTACAAGAGCAACCCGCGTCAAAAAATTTCTGAACGACTCA 4492
Db 3541 TAGTCCCGAGTACAAGAGCAACCCGCGTCAAAAAATTTCTGAACGACTCA 3600
Qy 4493 AACACCACTAGTACTTGTGTATCAGAGAAAAAATTGAAGCTCCCGTAAGAAATCG 4552
Db 3601 AACACCACTAGTACTTGTGTATCAGAGAAAAAATTGAAGCTCCCGTAAGAAATCG 3660
Qy 4553 AATGATCGCCCGATTTGGCATAGCCGGTGAGATAAGAACTACAACCTGGCTTCCGGT 4612
Db 3661 AATGATCGCCCGATTTGGCATAGCCGGTGAGATAAGAACTACAACCTGGCTTCCGGT 3720
Qy 4613 TTCCGCGCAGGACGGTACGACCTGGTTCATCAACATTGGAATAATAAGAAACC 4672
Db 3721 TTCCGCGCAGGACGGTACGACCTGGTTCATCAACATTGGAATAATAAGAAACC 3780
Qy 4673 ACCACTTTCAAGTGCAGAAAGACCATGCGCGCACTTAAAAACCCTTCCGCTTCGCCCC 4732
Db 3781 ACCACTTTCAAGTGCAGAAAGACCATGCGCGCACTTAAAAACCCTTCCGCTTCGCCCC 3840
Qy 4733 TGAATTGTTAACTCAGAGGCAACCCCTCGTGGTGAAGTCTATGGCTACGCCGACCGCA 4792
Db 3841 TGAATTGCTTAAACCAAGAGGCAACCCCTCGTGGTGAAGTCTATGGCTACGCCGACCGCA 3900
Qy 4793 ACAGTGAGAGAGTGTACCCGCTCTTGGCAGAAAGTTTGTCAAGGTGTCTGACAGCGAGAC 4852
Db 3901 ACAGTGAGAGAGTGTACCCGCTCTTGGCAGAAAGTTTGTCAAGGTGTCTGACAGCGAGAC 3960
Qy 4853 CAGATTGTCTCAAGCAATACAGAAATGTAAGTATTTCCGACAACTAGACAAACAGCC 4912
Db 3961 CAGATTGTCTCAAGCAATACAGAAATGTAAGTATTTCCGACAACTAGACAAACAGCC 4020
Qy 4913 GTACACGGCAATTCACCCCGCAACCATCTGAATTGCGTGAATTCGTCGGTATGAGGTA 4972
Db 4021 GTACACGGCAATTCACCCCGCAACCATCTGAATTGCGTGAATTCGTCGGTATGAGGTA 4080
Qy 4973 CAAGAGATGAGTTGGAGCCGCGCTCATACCGCAACCAAAAGGAGAAATATTGCTGACT 5032
Db 4081 CAAGAGATGAGTTGGAGCCGCGCTCATACCGCAACCAAAAGGAGAAATATTGCTGACT 4140
Qy 5033 GTCAAGAGAAAGAGTGTCAACGACGCCAATCCGCTGGTAGAACCGAGGAGAGTCT 5092
Db 4141 GTCAAGAGAAAGAGTGTCAACGACGCCAATCCGCTGGTAGAACCGAGGAGAGTCT 4200
Qy 5093 GCGGTGCATCTATAAAGTTGGCCGACCAAGTTTACCGATTCAAGCCACGAGACAGGCA 5152
Db 4201 GCGGTGCATCTATAAAGTTGGCCGACCAAGTTTACCGATTCAAGCCACGAGACAGGCA 4260
Qy 5153 CCGCAAGATGACTGTGTGCTAGAAAAGAAAGTATCCACGCGCTGATTTCC 5212
Db 4261 CCGCAAGATGACTGTGTGCTAGAAAAGAAAGTATCCACGCGCTGATTTCC 4320
Qy 5213 GGAAGCACCCAGACAGAAAGCCTTGAATTGCTACAAAAGCCTACCATGCAAGTGGCAG 5272
Db 4321 GGAAGCACCCAGACAGAAAGCCTTGAATTGCTACAAAAGCCTACCATGCAAGTGGCAG 4380
Qy 5273 ACTTAGTAATGAACATTAACATCAAGTCTGTGCCATTCCACTGCTATCTACAGGCAATT 5332
Db 4381 ACTTAGTAATGAACATTAACATCAAGTCTGTGCCATTCCACTGCTATCTACAGGCAATT 4440
Qy 5333 ACGCAGCCGGAAGAAGACCGCTTGAAGTATCACTTAAGTCTTGACAAACCGCTAGACA 5392
Db 4441 ACGCAGCCGGAAGAAGACCGCTTGAAGTATCACTTAAGTCTTGACAAACCGCTAGACA 4500
Qy 5393 GAAGTACGCGGACGTAAACCATCTATTGCTGGATGAAGTGAAGGAAGAATCGACG 5452
Db 4501 GAAGTACGCGGACGTAAACCATCTATTGCTGGATGAAGTGAAGGAAGAATCGACG 4560
Qy 5453 CGGCACTCAACTTAAGAGTCTGTAAACAGAGCTGAAGATGAAGATGAGATCGACG 5512

Db 4561 CGGCACTCCAATTAAAGAGTCTGTAAACAGAGCTGAAGATGAAGATATGAGATCGACG 4620
Qy 5513 ATGAGTTAGTATGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTA 5572
Db 4621 ATGAGTTAGTATGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTA 4680
Qy 5573 CAAAAGAAAAATTGATTCTGACTTCGAAGGCAACAAATTCATCAAGCAAGCAAAAGACA 5632
Db 4681 CAAAAGAAAAATTGATTCTGACTTCGAAGGCAACAAATTCATCAAGCAAGCAAAAGACA 4740
Qy 5633 TGGCGGAGATTAAGTCTGTTCCCTAAATGACCAAGAAAGTAATGAACAATGTGTGCT 5692
Db 4741 TGGCGGAGATTAAGTCTGTTCCCTAAATGACCAAGAAAGTAATGAACAATGTGTGCT 4800
Qy 5693 ACATATTGGTGAAGACCATGGAAGCAATCCGCAAAAGTGCCTCGACCATTAACCCGT 5752
Db 4801 ACATATTGGTGAAGACCATGGAAGCAATCCGCAAAAGTGCCTCGACCATTAACCCGT 4860
Qy 5753 CGTCTAGCCCGCAAAACGTTGCCGTGCTTTCATGTATGCCATGACGCCAGAAAGGG 5812
Db 4861 CGTCTAGCCCGCAAAACGTTGCCGTGCTTTCATGTATGCCATGACGCCAGAAAGGG 4920
Qy 5813 TCCACAGACTTGAAGCAATTAACGTCAAGAAAGTTACAGTATGCTCTCCACCCCTTC 5872
Db 4921 TCCACAGACTTGAAGCAATTAACGTCAAGAAAGTTACAGTATGCTCTCCACCCCTTC 4980
Qy 5873 CTAAGCAAAATTAAGATGTTCAAGAGTTCAAGAGTTACAGTATGCTCTCCACCCCTTC 5932
Db 4981 CTAAGCAAAATTAAGATGTTCAAGAGTTCAAGAGTTACAGTATGCTCTCCACCCCTTC 5040
Qy 5933 CGCACACTCCCGCATTCGTTCCCGCCGTAAGTACATAGAAGTGCAGAACAGCCTACCG 5992
Db 5041 CGCACACTCCCGCATTCGTTCCCGCCGTAAGTACATAGAAGTGCAGAACAGCCTACCG 5100
Qy 5993 CTCCTCTGCAAGGCGGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCAACATCTACAG 6052
Db 5101 CTCCTCTGCAAGGCGGAGGAGGCCCCCGAAGTTGTAGCGACACCGTCAACATCTACAG 5160
Qy 6053 CTGATTAACACTCGCTGTATGTCAACAGACTCTCACTGATATGATGACATAGCGAAG 6112
Db 5161 CTGATTAACACTCGCTGTATGTCAACAGACTCTCACTGATATGATGACATAGCGAAG 5220
Qy 6113 GCTCACTTTTTCAGACTTTAGCGGATCGGCAACTCTATTACTAGTATGACAAGTTGGT 6172
Db 5221 GCTCACTTTTTCAGACTTTAGCGGATCGGCAACTCTATTACTAGTATGACAAGTTGGT 5280
Qy 6173 CGTCAAGACCTAGTTCAGTAGAGTAGAGACCGAAGGACAGTGGTGGCTGACGTTTC 6232
Db 5281 CGTCAAGACCTAGTTCAGTAGAGTAGAGACCGAAGGACAGTGGTGGCTGACGTTTC 5340
Qy 6233 ATGCCGTCCAAGAGCCTGCCCTATTCCACCGCAAGGCTAAAGAAAGTGGCCGCTGG 6292
Db 5341 ATGCCGTCCAAGAGCCTGCCCTATTCCACCGCAAGGCTAAAGAAAGTGGCCGCTGG 5400
Qy 6293 CAGCGCAAGAAAAAGACCCACTCCACCGCAAGCAATAGCTGTAGTCCCTCAACTCT 6352
Db 5401 CAGCGCAAGAAAAAGACCCACTCCACCGCAAGCAATAGCTGTAGTCCCTCAACTCT 5460
Qy 6353 CTTTGTGGGTATCCATGTCCCTCGATCAATTTTCAGCGAGAGAGCGCCGCGCAGG 6412
Db 5461 CTTTGTGGGTATCCATGTCCCTCGATCAATTTTCAGCGAGAGAGCGCCGCGCAGG 5520
Qy 6413 CAGCGTACAAACCCCTGGCAACAGGCCCAAGATGTGCTATGTCTTCGATCGTTT 6472
Db 5521 CAGCGTACAAACCCCTGGCAACAGGCCCAAGATGTGCTATGTCTTCGATCGTTT 5580
Qy 6473 CCGACGAGAGATTGATGAGCTGAGCCGCAAGTAATGAGTCCGAACCCGTCTGTTG 6532
Db 5581 CCGACGAGAGATTGATGAGCTGAGCCGCAAGTAATGAGTCCGAACCCGTCTGTTG 5640
Qy 6533 GATCATTTGAACCGGGCGAAGTGAACCTCAATTATATGCTCCGATCAGCGTATCTTTTC 6592
Db 5641 GATCATTTGAACCGGGCGAAGTGAACCTCAATTATATGCTCCGATCAGCGTATCTTTTC 5700

QY	6593	CACTACGCAAGCAGAGACGTAGACGCGACGAGCAGAGGAACTGTAATACTGACTAAACCGGGG	6652
Db	5701	CACTACGCAAGCAGAGACGTAGACGCGACGAGCAGAGGAACTGTAATACTGACTAAACCGGGG	5760
QY	6653	TAGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAAGAGTCCGTTTC	6712
Db	5761	TAGTGGGTACATATTTTCGACGGACACAGGCCCTGGGCACTTGCAAAAAGAGTCCGTTTC	5820
QY	6713	TGCAGAACCAAGCTTACAGAAACCGACCTTGAGCGCAATGTCCTGAAAAGAAATTCATGCC	6772
Db	5821	TGCAGAACCAAGCTTACAGAAACCGACCTTGAGCGCAATGTCCTGAAAAGAAATTCATGCC	5880
QY	6773	CGGTGCTCGACACCGTCCGAAAGAGAACAACTCAAACCTCAGGTACCAGATGATGCCACCG	6832
Db	5881	CGGTGCTCGACACCGTCCGAAAGAGAACAACTCAAACCTCAGGTACCAGATGATGCCACCG	5940
QY	6833	AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAAGCCATAACCACTG	6892
Db	5941	AAGCCAACAAAAGTAGGTACCAGTCTCGTAAAGTAGAAAATCAGAAAAGCCATAACCACTG	6000
QY	6893	AGCGACTACTGTACAGACTACGACTGTATTAACCTCTGCCACAGATCAGCCAGAAATGCTATA	6952
Db	6001	AGCGACTACTGTACAGACTACGACTGTATTAACCTCTGCCACAGATCAGCCAGAAATGCTATA	6060
QY	6953	AGATCACCTATCCGAAACCATTTGTACTCCAGTAGCGTACC GGCGAACTACTCCGATCCAC	7012
Db	6061	AGATCACCTATCCGAAACCATTTGTACTCCAGTAGCGTACC GGCGAACTACTCCGATCCAC	6120
QY	7013	AGTTCGCTGTAGCTGTGTCTGTAAACAACCTATCTGCATGAGAACTATCCGACAGTAGACTTT	7072
Db	6121	AGTTCGCTGTAGCTGTGTCTGTAAACAACCTATCTGCATGAGAACTATCCGACAGTAGACTTT	6180
QY	7073	ATCAGATTACTGACGAGTAGATCGATGCTTACTTGATATGTTAGACGAGACAGTCCGATGCC	7132
Db	6181	ATCAGATTACTGACGAGTAGATCGATGCTTACTTGATATGTTAGACGAGACAGTCCGATGCC	6240
QY	7133	TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTA CCGAAAAACATGAGTATA	7192
Db	6241	TGGATACTGCAACCTTCTGCCCCGCTAAGCTTAGAAGTTA CCGAAAAACATGAGTATA	6300
QY	7193	GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAATGTGC	7252
Db	6301	GAGCCCCGAATATCCGCAGTGCGGTTCCATCAGCGATGCAGAACACGCTACAAATGTGC	6360
QY	7253	TCATTGCCGCACTAAAGAAATTGCAACGTCA CGCAGATGCGTGAACCTGCCAACACTGG	7312
Db	6361	TCATTGCCGCACTAAAGAAATTGCAACGTCA CGCAGATGCGTGAACCTGCCAACACTGG	6420
QY	7313	ACTCAGCGACATTCAATGTGCAATGCTTTGAAAATATGCA TGTATGACGAGTATTTGG	7372
Db	6421	ACTCAGCGACATTCAATGTGCAATGCTTTGAAAATATGCA TGTATGACGAGTATTTGG	6480
QY	7373	AGGAGTTCGCTCGAAGCCAAATTAGATTACCACTGAGTTTGTCA CCGCATATGTAGCTA	7432
Db	6481	AGGAGTTCGCTCGAAGCCAAATTAGATTACCACTGAGTTTGTCA CCGCATATGTAGCTA	6540
QY	7433	GACTGAAAAGCCCTAAGGCCCGCCCACTATTTTGCAAAAGCSTATA TTTGGTCCCATTTGC	7492
Db	6541	GACTGAAAAGCCCTAAGGCCCGCCCACTATTTTGCAAAAGCSTATA TTTGGTCCCATTTGC	6600
QY	7493	AAGAAAGTCCCTATGATAGATTGCTCATGAGCATGAAAAGAGACGTGAAAAGTTACACAG	7552
Db	6601	AAGAAAGTCCCTATGATAGATTGCTCATGAGCATGAAAAGAGACGTGAAAAGTTACACAG	6660
QY	7553	GCACGAAAACACAGAGAAGAAAGACCGAAAAGTACAAGTGTACAAGCCGACGAAACCCCTGG	7612
Db	6661	GCACGAAAACACAGAGAAGAAAGACCGAAAAGTACAAGTGTACAAGCCGACGAAACCCCTGG	6720
QY	7613	CGACTGCTTACTTATGCGGATTCACCGGGAATTAGTGCGTAA GCTTACGCGCTCTTG	7672
Db	6721	CGACTGCTTACTTATGCGGATTCACCGGGAATTAGTGCGTAA GCTTACGCGCGCTCTTG	6780

OY	7673	TTCCAAACATTCA CACGCTTTTGTGACATGTCGGCGGAGGATTTTGATGCATCATATAGCAG	7732
Db	6781	TTCCAAACATTCA CACGCTTTTGTGACATGTCGGCGGAGGATTTTGATGCATCATATAGCAG	6840
OY	7733	AACACTTCAAGCAAGGCGACC CGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC	7792
Db	6841	AACACTTCAAGCAAGGCGACC CGGTACTGGAGACGGATATCGCATCATTCGACAAAAGCC	6900
OY	7793	AAGACGACGCTATGGCGTTAACCGGCTGTGATGATCTTGAGGACCCTGGGTGGATCAAC	7852
Db	6901	AAGACGACGCTATGGCGTTAACCGGCTGTGATGATCTTGAGGACCCTGGGTGGATCAAC	6960
OY	7853	CAC TACTCGA CT TGATCGAGTGC GCTTTGGAGAAATATCATCCACC ATCTTA CCTACG	7912
Db	6961	CAC TACTCGA CT TGATCGAGTGC GCTTTGGAGAAATATCATCCACC ATCTTA CCTACG	7020
OY	7913	G TACTCGT TTAAATTCGGGGCGATGATGA AATCCGGAATGTTCTCTACA CTTTTTGTCA	7972
Db	7021	G TACTCGT TTAAATTCGGGGCGATGATGA AATCCGGAATGTTCTCTACA CTTTTTGTCA	7080
OY	7973	ACACAGTTTGAATGTC GTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACTCCA	8032
Db	7081	ACACAGTTTGAATGTC GTTATCGCCAGCAGAGTACTAGAAGAGCGGCTTAAAACTCCA	7140
OY	8033	GATGTGCAGCGTTCATTTGGCGACGACAACATCATACATGAGTAGTATCTGACAAAGAAA	8092
Db	7141	GATGTGCAGCGTTCATTTGGCGACGACAACATCATACATGAGTAGTATCTGACAAAGAAA	7200
OY	8093	TGGCTGAGAGGTGGCCACCTGGCTCAA CATGAGGTTAAGATCATCGACGAGTCATCG	8152
Db	7201	TGGCTGAGAGGTGGCCACCTGGCTCAA CATGAGGTTAAGATCATCGACGAGTCATCG	7260
OY	8153	GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTCGTTACTTCCACAG	8212
Db	7261	GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTCGTTACTTCCACAG	7320
OY	8213	CGTCCGCCGTGGCGGATCCCCGTGA AAAAGGCTGTTAAGTTGGGTA AACCGCTCCAGCCG	8272
Db	7321	CGTCCGCCGTGGCGGATCCCCGTGA AAAAGGCTGTTAAGTTGGGTA AACCGCTCCAGCCG	7380
OY	8273	ACGACGAGCAAGACGAAAGACAGAAAGACGCGCTCTGCTAGATGAAACAAAGCGCTGTTTA	8332
Db	7381	ACGACGAGCAAGACGAAAGACAGAAAGACGCGCTCTGCTAGATGAAACAAAGCGCTGTTTA	7440
OY	8333	GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA	8392
Db	7441	GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACAATA	7500
OY	8393	TTACACCTGTCTACTGGCACTTGAGAACTTTTGCCAGAGCAAAAAGACATTCCAAGCCA	8452
Db	7501	TTACACCTGTCTACTGGCACTTGAGAACTTTTGCCAGAGCAAAAAGACATTCCAAGCCA	7560
OY	8453	TCAGAGGGGAATAAAGCATCTCTACG GTGGTCC TTAATAGTCAGCATAGTACATTTTCAT	8512
Db	7561	TCAGAGGGGAATAAAGCATCTCTACG GTGGTCC TTAATAGTCAGCATAGTACATTTTCAT	7620
OY	8513	CTGACTAATACTACAACCA CCACCT 8539	
Db	7621	CTGACTAATACTACAACCA CCACCT 7647	

RESULT 14	
AAx77358	
ID	AAx77358 standard; DNA; 13905 BP.
XX	
AC	AAx77358;
XX	
DT	09-AUG-1999 (first entry)
XX	
DE	Polynucleotide sequence of PTES'2U.
XX	
KW	Nucleic acid identification; exogenous protein; gene sorting;
KW	growth factor; membrane receptor; sindbis virus; ss.

XX Synthetic.
OS
XX WO9925876-A1.
PN
XX 27-MAY-1999;
PD
XX 17-NOV-1998; 98WO-US024520.
PF
XX 17-NOV-1997; 97US-00972218.
PR
XX (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
PA
XX Bailey JE, Renner WA, Orberger GH, Koller D;
PI
XX WPI; 1999-357620/30.
DR
XX
XX
PT Isolating genes encoding proteins with selected properties, useful for
PT identifying therapeutic agents or targets.
PS
PS Disclosure; Fig 12A-D; 136pp; English.
XX
XX The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing a population of eukaryotic host cells, culturing the
CC cells under suitable conditions and identifying cells that contain the
CC recombinant nucleic acid. The method is used to sort genes according to
CC the type of proteins they express, and also to identify new ligand/
CC receptor interactions. Typical applications of the nucleic acid and the
CC exogenous protein are in isolation of new growth factors, cytokines,
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC which may be useful as therapeutic agents or therapeutic targets, e.g.
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC proliferation or metabolic processes etc. The protein can also be used to
CC screen for specific modulators. The nucleic acid can also be used as
CC sources of therapeutic antisense or ribozyme sequences. The method allows
CC the protein (rather than a partial DNA sequence) to be isolated and,
CC since a wide range of cells can be used, they can be expressed with the
CC correct glycosylation pattern
XX
SQ Sequence 13905 BP; 3931 A; 3551 C; 3440 G; 2983 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 2; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 893 ATTGACGGCGGTAGTACACACTATTGATCAACAGCCGACCAATTGCACTACCATCACA 952
Db 1 ATTGACGGCGGTAGTACACACTATTGATCAACAGCCGACCAATTGCACTACCATCACA 60
QY 953 TGGAGAACCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTGTGTGCAACTGC 1012
Db 61 TGGAGAACCCAGTAGTAAACGTAGACGTAGACCCCCAGAGTCCGTTGTGTGCAACTGC 120
QY 1013 AAAAAAGCTTCCGCAATTGAGTAGTACAGCAGGTCACTCCAAATGACCATGCTA 1072
Db 121 AAAAAAGCTTCCGCAATTGAGTAGTACAGCAGGTCACTCCAAATGACCATGCTA 180
QY 1073 ATGCCAGAGCATTTTCGATCTGCCAGTAACTAATCGAGCTGAGGTTCTACCAAG 1132
Db 181 ATGCCAGAGCATTTTCGATCTGCCAGTAACTAATCGAGCTGAGGTTCTACCAAG 240
QY 1133 CGACGATCTTGACATAGGACGACCGCGCTCGTAGAATGTTTCCGAGCACCACTATC 1192
Db 241 CGACGATCTTGACATAGGACGACCGCGCTCGTAGAATGTTTCCGAGCACCACTATC 300
QY 1193 ATTGTGTCTGCCCCATGCGTAGTCCAGAAAGACCCGACCGCATGATGAATAAGCCAGTA 1252
Db 301 ATTGTGTCTGCCCCATGCGTAGTCCAGAAAGACCCGACCGCATGATGAATAAGCCAGTA 360
QY 1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGATGAGAAATTAAAGATC 1312
Db 361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAGAACTTGATGAGAAATTAAAGATC 420

QY 1313 TCCGACCGTACTTGATACGCCCGGATGCTGAAACACCATCGCTCTGCTTTCAACAAGATG 1372
Db 421 TCCGACCGTACTTGATACGCCCGGATGCTGAAACACCATCGCTCTGCTTTCAACAAGATG 480
QY 1373 TTACCTGCAACATGCGTGCCGAATATTCGTCATGACGAGACGTGTATCAACGCTCCCG 1432
Db 481 TTACCTGCAACATGCGTGCCGAATATTCGTCATGACGAGACGTGTATCAACGCTCCCG 540
QY 1433 GAACATCTATCATCAGGCTATGAAAGCGCGGACCCCTGTACTGTGATTGGCTTCGACA 1492
Db 541 GAACATCTATCATCAGGCTATGAAAGCGCGGACCCCTGTACTGTGATTGGCTTCGACA 600
QY 1493 CCACCCAGTTCACTGTTCTCGGCTATGCGAGTTGTAACCTCGGTACAAACCACTGGG 1552
Db 601 CCACCCAGTTCACTGTTCTCGGCTATGCGAGTTGTAACCTCGGTACAAACCACTGGG 660
QY 1553 CCGACGAAAGTCTCTTGAAGCGCGTAACTCGGACTTTGACAGCAAAAGCTGAGTGAAG 1612
Db 661 CCGACGAAAGTCTCTTGAAGCGCGTAACTCGGACTTTGACAGCAAAAGCTGAGTGAAG 720
QY 1613 GTAGACAGAAATTTGTCGATAATGAGAGAAAGAGTTGAAGCCCGGTCGGGGTTT 1672
Db 721 GTAGACAGAAATTTGTCGATAATGAGAGAAAGAGTTGAAGCCCGGTCGGGGTTT 780
QY 1673 ATTTCTCCGTAGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAAGCTGGCATC 1732
Db 781 ATTTCTCCGTAGATCGACACTTTATCCAGAACACAGAGCCAGCTTGCAAGCTGGCATC 840
QY 1733 TTCCATCGGTGTTCCACTTGAATGAAAGCAGTGTACACTTCCGCTGTGATACAGTGG 1792
Db 841 TTCCATCGGTGTTCCACTTGAATGAAAGCAGTGTACACTTCCGCTGTGATACAGTGG 900
QY 1793 TGAGTTGCGAAGCTACGTAGTGAAGAAATCAACATCAGTCCCGGATCAAGGAGAAA 1852
Db 901 TGAGTTGCGAAGCTACGTAGTGAAGAAATCAACATCAGTCCCGGATCAAGGAGAAA 960
QY 1853 CCGTGATACGCGGTTACACACAAATAGCAGGGCTTCTGTATGCAAAAGTTACTGACA 1912
Db 961 CCGTGATACGCGGTTACACACAAATAGCAGGGCTTCTGTATGCAAAAGTTACTGACA 1020
QY 1913 CAGTAAAGAGAAACGGGTATCGTTCCTGTGTGTCACGTCATCCCGGCCACCATATGCG 1972
Db 1021 CAGTAAAGAGAAACGGGTATCGTTCCTGTGTGTCACGTCATCCCGGCCACCATATGCG 1080
QY 1973 ATCAGATGACTGTATATATGCCCACGATATATCACTGACGATGCAAAAACTTCTGG 2032
Db 1081 ATCAGATGACTGTATATATGCCCACGATATATCACTGACGATGCAAAAACTTCTGG 1140
QY 2033 TTGGCTCAACGAGCAATTGTCTATTAACGTTAGACTTAACAGAAACCAACCATGTC 2092
Db 1141 TTGGCTCAACGAGCAATTGTCTATTAACGTTAGACTTAACAGAAACCAACCATGTC 1200
QY 2093 AAATTAACCTTCTCCGATCATAGCACAAGGTTACGAATGGGCTTAAGAGCGCAAG 2152
Db 1201 AAATTAACCTTCTCCGATCATAGCACAAGGTTACGAATGGGCTTAAGAGCGCAAG 1260
QY 2153 ATGATCTTGATTAAGAGAAATGCTGGTACTAGAGAACGCAAGCTTAAGTATGGCTGT 2212
Db 1261 ATGATCTTGATTAAGAGAAATGCTGGTACTAGAGAACGCAAGCTTAAGTATGGCTGT 1320
QY 2213 TGTGGGCGTTTCGACTAAGAAAGTACATTGTTTATGCCCCACCTGAAACGAGACCT 2272
Db 1321 TGTGGGCGTTTCGACTAAGAAAGTACATTGTTTATGCCCCACCTGAAACGAGACCT 1380
QY 2273 GCGTAAAGTCCAGCCTCTTTTAAAGCTTTTCCATGTGTCGTAAGAGCACTCTT 2332
Db 1381 GCGTAAAGTCCAGCCTCTTTTAAAGCTTTTCCATGTGTCGTAAGAGCACTCTT 1440
QY 2333 TGCCCATGTGCTGAGGACAGAAATTGAACTGGCATTGCAACCAAGAAAGAGAAAAAC 2392
Db 1441 TGCCCATGTGCTGAGGACAGAAATTGAACTGGCATTGCAACCAAGAAAGAGAAAAAC 1500

QY	2393	TGCTGAGGCTCGAGGAATTAGTCATGAGGCCAAGGCTGCTTTTGAGATGCTCAGG	2452
	1501	TGCTGAGGCTCGAGGAATTAGTCATGAGGCCAAGGCTGCTTTTGAGATGCTCAGG	1560
QY	2453	AGGAAGCCAGAGCGGAGAGCTCCGAGAAGCACTTCCACATTAGTGACAGACAAAGCA	2512
Db	1561	AGGAAGCCAGAGCGGAGAGCTCCGAGAAGCACTTCCACATTAGTGACAGACAAAGCA	1620
QY	2513	TCGAGGACGCCGAGAGTTGTTCTGCGAAGTGGAGGGGCTCCAGGCGACATCGGACAG	2572
Db	1621	TCGAGGACGCCGAGAGTTGTTCTGCGAAGTGGAGGGGCTCCAGGCGACATCGGACAG	1680
QY	2573	CATTAGTTGAAACCCCGCGGTCACGTAAGGATATACCTCAAGCAATGACCGTATGA	2632
Db	1681	CATTAGTTGAAACCCCGCGGTCACGTAAGGATATACCTCAAGCAATGACCGTATGA	1740
QY	2633	TCGGACAGTATATCGTTGTCTCGCCAAACTGTGTCTGAAGAATGCCAACTCGACACG	2692
Db	1741	TCGGACAGTATATCGTTGTCTCGCCAAACTGTGTCTGAAGAATGCCAACTCGACACG	1800
QY	2693	CGCAACCCGCTAGCAGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGTACG	2752
Db	1801	CGCAACCCGCTAGCAGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGTACG	1860
QY	2753	CGGTGGAACCATACGACGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAG	2812
Db	1861	CGGTGGAACCATACGACGCTAAAGTACTGATGCCAGCAGAGGTGCCGTACCATGGCCAG	1920
QY	2813	AATTCCTAGCACTGAGTGAGACGCCACGTTAGTGTACACGAAGAAGAGTTGTGAACC	2872
Db	1921	AATTCCTAGCACTGAGTGAGACGCCACGTTAGTGTACACGAAGAAGAGTTGTGAACC	1980
QY	2873	GCAAACTATACCACATTTGCCATGTCATGCCCCGCCCAAGAAITACAGAAGAGGACGATACA	2932
Db	1981	GCAAACTATACCACATTTGCCATGTCATGCCCCGCCCAAGAAITACAGAAGAGGACGATACA	2040
QY	2933	AGGTTACAAAAGGACAGACTTGCAGAAAACAGAGTACGTGTTTGAAGTGACAAAGACGTT	2992
Db	2041	AGGTTACAAAAGGACAGACTTGCAGAAAACAGAGTACGTGTTTGAAGTGACAAAGACGTT	2100
QY	2993	GCGTTAAGAAAGAAAGCCTCAGGTCTGTCCTCTCGGAGAACTGACCAACCTCCT	3052
Db	2101	GCGTTAAGAAAGAAAGCCTCAGGTCTGTCCTCTCGGAGAACTGACCAACCTCCT	2160
QY	3053	ATCATGAGCTAGCTCTGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAAGTGGAAA	3112
Db	2161	ATCATGAGCTAGCTCTGAGGGACTGAAGACCCGACCTGCGGTCCCGTACAAAGTGGAAA	2220
QY	3113	CAATAGGAGTATAGGCACACCGGGGTCCGGCAAGTCAGCTATTATCAAGTCAACTGTCA	3172
Db	2221	CAATAGGAGTATAGGCACACCGGGGTCCGGCAAGTCAGCTATTATCAAGTCAACTGTCA	2280
QY	3173	CGGCACGAGATCTTGTTCACAGCGGAAAGAAATTTGTCCGAAATTGAGGCCGACG	3232
Db	2281	CGGCACGAGATCTTGTTCACAGCGGAAAGAAATTTGTCCGAAATTGAGGCCGACG	2340
QY	3233	TGCTAAGACTGAGGGGTATGAGATTACGTGGAAGACAGTAGATTCCGTTATGCTCAAG	3292
Db	2341	TGCTAAGACTGAGGGGTATGAGATTACGTGGAAGACAGTAGATTCCGTTATGCTCAAG	2400
QY	3293	GATGCCACAAAGCCGTAGAACTGCTGTACGTTGACGAAGCGTTCCGTGCCACGCGAGAG	3352
Db	2401	GATGCCACAAAGCCGTAGAACTGCTGTACGTTGACGAAGCGTTCCGTGCCACGCGAGAG	2460
QY	3353	CACACTTGCCCTTGATTGCTATCGTCAGGCCCCGCAAGAGGTAGTACTATGCGGAGACC	3412
Db	2461	CACACTTGCCCTTGATTGCTATCGTCAGGCCCCGCAAGAGGTAGTACTATGCGGAGACC	2520
QY	3413	CCATGCAATGCGGATTTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCCTGAAA	3472
Db	2521	CCATGCAATGCGGATTTCTTCAACATGATGCAACTAAAGGTACATTTCAATCACCCCTGAAA	2580
QY	3473	AAGACATATGCAACCAAGACATTTCAAGTATATCTCCCGCGCTTGACACACAGCCAGTTA	3532

Db	2581	AAGACATATGCAACCAAGACATTCTACAGATATATCTCCCGCGCTTGCAACAGCCAGTTA	2640
QY	3533	CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAACCACGAACCCGTGCAAGA	3592
Db	2641	CAGCTATTGTATCGACACTGCATTACGATGGAAAGATGAAACCACGAACCCGTGCAAGA	2700
QY	3593	AGAACATTGAAATCGATATTACAGGGGGCCCAAAAGCCGAAAGCCAGGGGATATCATCTGA	3652
Db	2701	AGAACATTGAAATCGATATTACAGGGGGCCCAAAAGCCGAAAGCCAGGGGATATCATCTGA	2760
QY	3653	CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAAATCGACTATCCCGGACATGAAGTAATGA	3712
Db	2761	CATGTTTCCGCGGGTGGGTTAAGCAATTGCAAAATCGACTATCCCGGACATGAAGTAATGA	2820
QY	3713	CAGCCGCGGCTCACAAGGGCTAACCAAGAAAGAGTGTATGCCGTCCGGCAAAAAGTCA	3772
Db	2821	CAGCCGCGGCTCACAAGGGCTAACCAAGAAAGAGTGTATGCCGTCCGGCAAAAAGTCA	2880
QY	3773	ATGAAACCCTACTGTACGGGATCACATCAGACATGTGAACGTGTTGTCACCCGCACTG	3832
Db	2881	ATGAAACCCTACTGTACGGGATCACATCAGACATGTGAACGTGTTGTCACCCGCACTG	2940
QY	3833	AGGACAGGCTAGTGTGGAAAACTTGCAGGGCGAACCCATGGATTAAAGCCCCACTAACA	3892
Db	2941	AGGACAGGCTAGTGTGGAAAACTTGCAGGGCGAACCCATGGATTAAAGCCCCACTAACA	3000
QY	3893	TACCTAAAGGAACCTTTACAGGCTACTATAGAGACTGGGAAGCTGAACACAGGGAATAA	3952
Db	3001	TACCTAAAGGAACCTTTACAGGCTACTATAGAGACTGGGAAGCTGAACACAGGGAATAA	3060
QY	3953	TTGCTGCAATTAACAGCCCCCACTCCCCGTGCCAATCCGTTACGCTGCAAGCAACGTTT	4012
Db	3061	TTGCTGCAATTAACAGCCCCCACTCCCCGTGCCAATCCGTTACGCTGCAAGCAACGTTT	3120
QY	4013	GCTGGCGAAAGCAATTGGAACCGATACTAGCCACGGCCGATTCGTACTTAACCGGTTGCC	4072
Db	3121	GCTGGCGAAAGCAATTGGAACCGATACTAGCCACGGCCGATTCGTACTTAACCGGTTGCC	3180
QY	4073	AGTGAGCGCACTGTTCCACAGTTTGGCGGATGACAACACCATTCGGCCATTACGCCCT	4132
Db	3181	AGTGAGCGCACTGTTCCACAGTTTGGCGGATGACAACACCATTCGGCCATTACGCCCT	3240
QY	4133	TAGACGTAATTTGCAATTAAGTTTTCGGCATGGACTTGACAAAGCCGACTGTTTCTAAAC	4192
Db	3241	TAGACGTAATTTGCAATTAAGTTTTCGGCATGGACTTGACAAAGCCGACTGTTTCTAAAC	3300
QY	4193	AGAGCATCCCACTAACGTACCATCCCCCGCATTCAGCGAGGCGCGTAGCTATTGGGACA	4252
Db	3301	AGAGCATCCCACTAACGTACCATCCCCCGCATTCAGCGAGGCGCGTAGCTATTGGGACA	3360
QY	4253	ACAGCCCAAGAACCCGCAAGTATGGGTACGATCAGCCATTGCCGCCGAATCTCCCGTA	4312
Db	3361	ACAGCCCAAGAACCCGCAAGTATGGGTACGATCAGCCATTGCCGCCGAATCTCCCGTA	3420
QY	4313	GATTTCCGAGTTCAGCTAGCTGGAAAGGCAACAATTGATTGTCAGCGGGAGAA	4372
Db	3421	GATTTCCGAGTTCAGCTAGCTGGAAAGGCAACAATTGATTGTCAGCGGGAGAA	3480
QY	4373	CCAGAGTTATCTTGCAACAGCATTAACCTGTCGCCGTGAACCCGAATCTTCTCACGCCCT	4432
Db	3481	CCAGAGTTATCTTGCAACAGCATTAACCTGTCGCCGTGAACCCGAATCTTCTCACGCCCT	3540
QY	4433	TAGTCCCCGAGTACAGGAGAACCAACCCCGCGTCAAAAAATTCTTGAACCAAGTTCA	4492
Db	3541	TAGTCCCCGAGTACAGGAGAACCAACCCCGCGTCAAAAAATTCTTGAACCAAGTTCA	3600
QY	4493	AACACCACTCAGTACTGTGTATCAGAGGAAAAATTGAAGCTCCCGTAAAGAAATCG	4552
Db	3601	AACACCACTCAGTACTGTGTATCAGAGGAAAAATTGAAGCTCCCGTAAAGAAATCG	3660
QY	4553	AATGATCGCCCGATTGGCATAGCCCGGTGAGATAAGAACTACAACTGCTTCCGGT	4612

Db 3661 AATGATCGCCCCGATTGGCATAGCCGGTGAGATAGAATACTACAACCTGGCTTTCGGGT 3720
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QY 4673 ACCACTTTACAGAGTGCAGAGACCATGCGGGACCTTAAAAACCTTTCCGCTTCGGCCC 4732
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QY 4733 TGAATGTTTAACTCAGAGGACCCCTCGTGTGAAGTCCCTATGGCTACGCCGACCGCA 4792
Db 3841 TGAATGCTTAACTCAGAGGACCCCTCGTGTGAAGTCCCTATGGCTACGCCGACCGCA 3900
QY 4793 ACAGTGAGAGCTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAAGGTGTCTGACGCGAGAC 4852
Db 3901 ACAGTGAGAGCTAGTCAACCGCTCTTGCCAGAAAGTTTGTCAAGGTGTCTGACGCGAGAC 3960
QY 4853 CAGATTGTGTCTCAAGCAATACAGAAATGTAACCTGATTTTCCGACAATAAGACAACAGCC 4912
Db 3961 CAGATTGTGTCTCAAGCAATACAGAAATGTAACCTGATTTTCCGACAATAAGACAACAGCC 4020
QY 4913 GTACACGGCAATTCACCCCGCACCATTGTAAATTGCGTATTTCCGCTGTATGAGGTA 4972
Db 4021 GTACACGGCAATTCACCCCGCACCATTGTAAATTGCGTATTTCCGCTGTATGAGGTA 4080
QY 4973 CAAGAGATGAGTTGAGCCGCGCGCTCATACCGCACCAAAAGGAGAAATATTGCTGACT 5032
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QY 5093 GCCGTGCCATCTATAAACCTTGCGCCGACCACTTTTACCAGATTCAAGCCACGAGACAGGCA 5152
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Db 7441 GAGTAGGTATAACAGGCACTTTAGCAGTGGCCGTGACGACCCCGTATGAGGTAGACATA 7500
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QY 8453 TCAGAGGGGAAATTAAGCATCTCTACGGTGTCTTAAATAGTCAGCATAGTACATTTCA 8512
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Db 7561 TCAGAGGGGAAATTAAGCATCTCTACGGTGTCTTAAATAGTCAGCATAGTACATTTCA 7620
QY 8513 CTGACTAATACTACAAACCAACCACT 8539
| | | | |
Db 7621 CTGACTAATACTACAAACCAACCACT 7647

RESULT 15
AAA90390
ID AAA90390 standard; DNA; 13905 BP.
XX AC AAA90390;
XX DT 10-JAN-2001 (first entry)
XX DE Plasmid pTES'2J DNA sequence.
XX KW Nucleic acid identification; exogenous protein; drug screening;
XX KM recombinant expression; pTES'2J; cyclic; circular; ds.
OS Synthetic.
XX OS
XX PN JF2000189173-A.
XX PD 11-JUL-2000.
XX PF 23-AUG-1999; 99JP-00236220.
XX PR 17-NOV-1998; 98US-00193707.
XX PR 17-NOV-1998; 98WO-US024520.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.

XX
DR WPI: 2000-551637/51.
XX
PT Identifying a recombinant nucleic acid to identify and isolate various
PT cellular proteins, comprises culturing a composition comprising
PT eukaryotic host cells and identifying a cell comprising recombinant
PT nucleic acid.
XX
PS Example: Fig 12A-D; 56pp; Japanese.
XX
CC The invention relates to the identification of a recombinant nucleic acid
CC encoding an exogenous protein having a selected property. The method
CC comprises preparing populations of eukaryotic host cells, where each cell
CC comprises an expression vector encoding a different exogenous protein.
CC The host cells are cultured under suitable conditions and the nucleic
CC acid which encodes the exogenous protein is identified. The method is
CC useful for the identification and isolation of proteins with a selected
CC property. Typical applications of the nucleic acid and the exogenous
CC protein are in isolation of new growth factors, cytokines, membrane
CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
CC apoptotic or tumour suppressing proteins, regulators of cell
CC proliferation or of metabolic processes. The protein can also be used to
CC screen for ligands and specific modulators of activity. The method of the
CC invention allows the direct cloning of full length cDNAs in one step. It
CC facilitates direct expression of the protein without the need to perform
CC further procedures such as subcloning and establishment of a cell line
CC for protein production. The method allows a protein of interest (rather
CC than a partial DNA sequence) to be isolated and, since a wide range of
CC cell types can be used, they can be expressed in a correctly folded and
CC glycosylated form. The present sequence represents plasmid pTB5'2J which
CC was used in the exemplifications of the invention. This patent is related
CC to WO925876
SQ Sequence 13905 BP; 3931 A; 3551 C; 3440 G; 2983 T; 0 U; 0 Other;
Query Match 89.4%; Score 7637.4; DB 3; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 893 ATTGACGGCGTAGTACACACTATTGAAATCAACAGCCGCAATTGCACTACATCACAA 952
DB 1 ATTGACGGCGTAGTACACACTATTGAAATCAACAGCCGCAATTGCACTACATCACAA 60
QY 953 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCGACAGTCCGTTGTCGTGCAACTGC 1012
DB 61 TGGAGAAGCCAGTAGTAAACGTAGACGTAGACCCCGACAGTCCGTTGTCGTGCAACTGC 120
QY 1013 AAAAAAGCTTCCCGCAATTGAGTAGTAGACAGCAGGTCACTCCAAATGACCATGCTA 1072
DB 121 AAAAAAGCTTCCCGCAATTGAGTAGTAGACAGCAGGTCACTCCAAATGACCATGCTA 180
QY 1073 ATGCCAGAGCATTTTCGCATCTGGCCAGTAACTAATCGAGCTGGAGGTTCTTACCACAG 1132
DB 181 ATGCCAGAGCATTTTCGCATCTGGCCAGTAACTAATCGAGCTGGAGGTTCTTACCACAG 240
QY 1133 CGACGATCTTGGACATAGGCGAGCGCAGCGGCTGCTAGAAATGTTTCCGAGCAGCATATC 1192
DB 241 CGACGATCTTGGACATAGGCGAGCGCAGCGGCTGCTAGAAATGTTTCCGAGCAGCATATC 300
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QY 1553 CCGACGAGAAAGTCTTGAAGCGCGTAACTCGCACTTTGCAGCACAAAGCTGAGTGAAG 1612
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